

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Laurin Wells Examiner #: 75202 Date: 4/15/02
 Art Unit: 1017 Phone Number 30 151542 Serial Number: 01157276
 Mail Box and Bldg/Room Location: 3012 Results Format Preferred (circle): PAPER DISK. E-MAIL

If more than one search is submitted, please prioritize searches in order of need. MEJ

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

SEQ ID NO: 1032

→ therapeutic peptide

Point of Contact:
 Toby Port
 Technical Info. Specialist
 CM1 6A04
 703-308-3634

RECEIVED
 APR - 5 2002
 (STIC)

prot 1032

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) _____	STN _____	
Searcher Phone #: _____	AA Sequence (#) <u>1</u>	Dialog <u>3</u>	
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____	
Date Searcher Picked Up: <u>4/15</u>	Bibliographic _____	Dr. Link _____	
Date Completed: <u>4/8</u>	Litigation _____	Lexis/Nexis _____	
Searcher Prep & Review Time: <u>10</u>	Fulltext _____	Sequence Systems <u>CS</u>	
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____	
Online Time: <u>10</u>	Other _____	Other (specify) _____	

Query Match 100.0%; Score 138; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 6.9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRRFCGALIHARFVMTAASCF 25
|||||
DB 20 NOGRRFCGALIHARFVMTAASCF 44

RESULT 12
US-08-944-483-32
Sequence 32, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRADOS, EDWARD H.
APPLICANT: KLAS, MICHAEL R.
APPLICANT: KUSSEL, JENNIFER D.
APPLICANT: STRAUSS, JENNIFER D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
FILING DATE:
PRIORITY:
CLASSIFICATION: A24
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SOURCE CHARACTERISTICS:
SEQUENCE: 225 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-08-944-483-32

Query Match 100.0%; Score 138; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 7e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRRFCGALIHARFVMTAASCF 25
|||||
DB 20 NOGRRFCGALIHARFVMTAASCF 44

RESULT 13
US-09-258-934-38
Sequence 38, Application US/09258934
Patent No. 6107460
GENERAL INFORMATION:
APPLICANT: Anne Pereira
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 5864,002
CURRENT APPLICATION NUMBER: US/09/258,934
CURRENT FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 58
SOFTWARE: WordPerfect 5.1 (saved in ASCII format) *Software*
SEQ ID NO 38
LENGTH: 25
TYPE: PPT
ORGANISM: homo sapien
US-09-258-934-38

Query Match 99.3%; Score 137; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.2e-13;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRRFCGALIHARFVMTAASCF 25
|||||
DB 1 NOGRRFCGALIHARFVMTAASCF 25

RESULT 14
US-09-258-934-36
Sequence 36, Application US/09258934
Patent No. 6107460
GENERAL INFORMATION:
APPLICANT: Anne Pereira
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 5864,002
CURRENT APPLICATION NUMBER: US/09/258,934
CURRENT FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 58
SOFTWARE: WordPerfect 5.1 (saved in ASCII format) *Software*
SEQ ID NO 36
LENGTH: 25
TYPE: PPT
ORGANISM: homo sapien
US-09-258-934-36

Query Match 97.8%; Score 135; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.2e-13;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRRFCGALIHARFVMTAASCF 25
|||||
DB 1 NOGRRFCGALIHARFVMTAASCF 25

RESULT 15
US-09-258-934-37
Sequence 37, Application US/09258934
Patent No. 6107460
GENERAL INFORMATION:
APPLICANT: Anne Pereira
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 5864,002
CURRENT APPLICATION NUMBER: US/09/258,934
CURRENT FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 58
SOFTWARE: WordPerfect 5.1 (saved in ASCII format) *Software*
SEQ ID NO 37
LENGTH: 25
TYPE: PPT
ORGANISM: homo sapien
US-09-258-934-37

Fri Apr 5 15:13:00 2002

us-09-657-276-1032.rai

Page 4

OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: WordPerfect 5.1 (saved in ASCII format)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/260,373
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,328
FILING DATE: 08/25/1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,931
FILING DATE: October 30, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,417
FILING DATE: March 18, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/543,151
FILING DATE: June 25, 1990
PRIOR APPLICATION DATA: 07/775,739
APPLICATION NUMBER:
FILING DATE: July 5, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Corbett, Christopher W., Ph.D.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 5E20,360
TELECOMMUNICATION INFORMATION:
TELEPHONE: 405-478-5349
TELEFAX: 405-478-5349
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TOPLOC: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
US-09-260-373-1

Query Match 100.0%; Score 138; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 8,3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOGRRFGCALIHARFVMTASCRQ 25
DB 1 NOGRRFGCALIHARFVMTASCRQ 25

RESULT 7
US-09-258-934-1
Sequence 1, Application US/09258934
Patent No. 6107460
GENERAL INFORMATION:
APPLICANT: Anne Peretia
TITLE OF INVENTION: ANTICATABOLIC PEPTIDES AND METHODS OF USE THEREOF
FILE REFERENCE: 5864,002
CURRENT APPLICATION NUMBER: US/09/258,934
CURRENT FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 58
SOFTWARE: WordPerfect 5.1 (saved in ASCII format) *Software*
SEQ ID NO 1
LENGTH: 25
TYPE: PRT
ORGANISM: homo sapien
US-09-258-934-1

Query Match 100.0%; Score 138; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 8,3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOGRRFGCALIHARFVMTASCRQ 25
|||||

DB 1 NOGRRFGCALIHARFVMTASCRQ 25
RESULT 8
US-08-925-708-1
Sequence 1, Application US/08925708
Patent No. 5939390
GENERAL INFORMATION:
APPLICANT: Floodard, Hans
TITLE OF INVENTION: A Pharmaceutical Composition
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5939390d1sk of No. 5939390th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastISO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,708
FILING DATE: 9-SEPT-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Rasmussen, Paul
REGISTRATION NUMBER: 14,086
REFERENCE/DOCKET NUMBER: 4119,204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPLOC: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Source
ORIGINAL SOURCE: human
US-08-925-708-1

Query Match 100.0%; Score 138; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 6,9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOGRRFGCALIHARFVMTASCRQ 25
DB 20 NOGRRFGCALIHARFVMTASCRQ 44

RESULT 9
US-07-969-931-9
Sequence 9, Application US/07969931
Patent No. 5458874
GENERAL INFORMATION:
APPLICANT: Peretia, Heloise Anne
TITLE OF INVENTION: Anticatabolic, Antiprotic and
ATLASANT INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 133 Carnegie Way N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303

```
Query Match          100.0%: Score 138; DB 1; Length 25;
Best Local Similarity 100.0%: Pred. No. 8.3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRHFGGALIHARFVMTASCFQ 25
DB 1 NOGRHFGGALIHARFVMTASCFQ 25

RESULT 2
US-07-855-417A-8
: Sequence 8, Application US/07855417A
: Patent No. 5484885
: GENERAL INFORMATION:
: APPLICANT: Perreira, Heloise Anne
: APPLICANT: Spletznagel, John K.
: TITLE OF INVENTION: Chemotactic, Antibiotic and
: TITLE OF INVENTION: Lipopolysaccharide-binding Peptide Fragments of CAP37
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS: Rosenberg, P.C.
: ADDRESS: 1050 N. 15th Street, Suite 400
: STREET: 113 Carnegie Way N.W., Suite 400
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/855,417A
: FILING DATE: 18-MAR-1992
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/543,151
: FILING DATE: 25-JUN-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/375,739
: FILING DATE: 05-JUL-1989
: ATTORNEY/AGENT INFORMATION:
: REGISTRATION NUMBER: 14,927
: REFERENCE/DOCKET NUMBER: 0510,024
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 688-9880
: TELEFAX: (404) 688-9880
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
US-07-855-417A-8

Query Match          100.0%: Score 138; DB 1; Length 25;
Best Local Similarity 100.0%: Pred. No. 8.3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRHFGGALIHARFVMTASCFQ 25
DB 1 NOGRHFGGALIHARFVMTASCFQ 25

RESULT 3
US-08-235-399-1
: Sequence 1, Application US/08235399
: Patent No. 5607916
: GENERAL INFORMATION:
: APPLICANT: Perreira, Heloise Anne
: APPLICANT: Lerner, Megan R.
: TITLE OF INVENTION: Method and Composition for the Treatment
: TITLE OF INVENTION: of Septic Shock
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESS: Christopher W. Corbett, Ph.D.
: ADDRESS: Dunlap, Coddling & Lee, P.C.
: STREET: 400 No. 5607916th Broadway, Suite 420
: CITY: Oklahoma City
: STATE: Oklahoma
: COUNTRY: United States of America
: ZIP: 73114
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5, 1.44 Mb High Density Diskette
: OPERATING SYSTEM: MS-DOS 5.00
: SOFTWARE: WordPerfect 5.1 (saved in ASCII format)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 09/08/235,399
: FILING DATE: July 5, 1989
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,931
: FILING DATE: October 30, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/855,417
: FILING DATE: March 18, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/543,151
: FILING DATE: June 25, 1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/375,739
: FILING DATE: July 5, 1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Christopher W. Corbett, Ph.D.
: REGISTRATION NUMBER: 36,109
: REFERENCE/DOCKET NUMBER: 5820,291
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 405-478-5344
: TELEFAX: 405-478-5349
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
US-08-235-399-1

Query Match          100.0%: Score 138; DB 1; Length 25;
Best Local Similarity 100.0%: Pred. No. 8.3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRHFGGALIHARFVMTASCFQ 25
DB 1 NOGRHFGGALIHARFVMTASCFQ 25

RESULT 4
US-08-482-328-1
: Sequence 1, Application US/08482328
: Patent No. 5627262
: GENERAL INFORMATION:
: APPLICANT: Perreira, Heloise Anne
: APPLICANT: Dunlap, Coddling & Lee, P.C.
: TITLE OF INVENTION: Method and Composition for the Treatment
: TITLE OF INVENTION: of Septic Shock
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESS: Christopher W. Corbett, Ph.D.
: ADDRESS: Dunlap & Coddling, P.C.
```

Fri Apr 5 15:13:01 2002

us-09-657-276-1032.rsp

Page 6

CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: A6003792; M0537469.1; -.
DR EMBL: A0081033; M0537469.1; -.
DR EMBL: F040034507; G011192.
DR InterPro: IPR001314; ChymoCrpsn.
DR InterPro: IPR001354; Trypsin.
DR Pfam: P00089; Crpsn_1.
DR PRINTS: PR00722; CHMOTRPSIN.
DR SMART: S00002; CHMOTRPSIN.
DR PROSITE: PS00134; TRYPsin_HIS. 1.
DR PROSITE: PS00135; TRYPsin_SER. 1.
KM Hydrolase: Serine protease.
KO SEQUENCE 269 AA: 28837 MW: 9797839B/0ECD318 CRC64:

```

0y      2  GCGAGCGCATGATPMTAAASERO 25
        ||||| ||||| |
Db      38  GCGHGGCAGTIGIDVLTAAACEE 61
          Matches   15; Conservative   3; Mismatches   6; Indels   0; Gaps   0;
          Boot Match 60.1%; Score 83; DB Size Length 269;
          Query Local Similarity 62.5%; Pred. No. 1,3e-05;

```

```

RESULT 13
013208 PRELIMINARY: PRT: 567 AA.
ID 013208
AC 013208
DT 01-NOV-1996 (REMBREL_01, Created)
DT 01-JUN-1998 (REMBREL_01, Sequence update)
DT 01-JUN-2003 (REMBREL_17, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN HOMOLOG (DIPSLIA).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae;
OX NCBI_Taxid:9606;
RN [1]
RA SEQUENCE FROM N.A.
RP Degen S.J.F., McDowell J.S.A., Walz S.E., Gould F., Stuart L.A., Carril B.;
RC Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RL SHARP SHOTGUN SEQUENCING OF RAT PROTEASES, TRYPsin FAMILY.
DS EMBL:U00054; JNCI63923.1;
DR HSP: p00747; ZPK4.
DR MEMOPS: S01.977; -.
DR InterPro: IPR000001; Krtingle.
DR InterPro: IPR001014; PAN.
DR InterPro: IPR003609; pan_app.
DR InterPro: IPR001254; trypsin.
DR Pfam: PF00051; Krtingle_4.
DR Pfam: PF00024; PAN_1.
DR Pfam: PF00018; trypsin_1.
DR Prosite: PS00031; KR_4.
DR SMART: SM00130; KR_4.
DR SMART: SM00473; PAN_AP_1.
DR SMART: PS00031; KRINGLE_1_2.
DR Prosite: PS00070; KRINGLE_2_4.
DR Hydrobase: Serine protease.
SC SEQUENCE 567 AA; 6416 MW; 3FC3BB07F1645810 CRC64;
```

Query Match	60.1%	Score 83	DB 4	Length 567
Post Local Similarity	52.2%	Pred. NO. 2.7e-05		
Matches 12: Conservative	7	Mismatches 4	Indels 0	Gaps 0
0Y	2	CGGATTCGAGATTAATGTTATACATG	24	
	0	:		
DB	477	CGGGTCGGAGTACGCTATTAATGCT	499	

ID	OSRiv4_	PRELIMINARY:	PRT:	648 AA.
D7	01-MAR-2001	(TREMBLEL_16_Created)		
D7	01-MAR-2001	(TREMBLEL_16_Last sequence update)		
D7	01-JUN-2001	(TREMBLEL_16_Last sequence update)		
D7	01-AUG-2003	(STRICKEL TO MS1) (MACROPHAGE STIMULATING 1 (HEPATOCYTE		
D7	DIFFERENTIAL LINK))			
CX	DJ118241.3			
OS	Homo sapiens (Human).			
OC	Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;			
NCBI	Nematoda; Euteleostei; Primates; Cetartiodactyla; Homiinidae; Homo;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bld C.;			
RL	Submitted (NOV-2000) to the EMBL/Genbank/DDBB databases.			
CC	-1- SIMILARITY: TO SERINE PROTEASES., TRYPSIN FAMILY.			
CC	-1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).			
DR	EMBL: AL137798: GAGT639.1			
DR	Interpro: IPRO01314: Chymotrypsin.			
DR	Interpro: IPRO03014: PAH angle.			
DR	Interpro: IPRO03609: Pan_app.			
DR	Interpro: IPRO01254: Trypsin.			
DR	Pfam: PF00051: kringle_4.			
DR	Pfam: PF00024: PAN_1.			
DR	Pfam: PFO0089: trypsin_1.			
DR	PRINTS: PR00722: CHYMOTRYPSIN.			
DR	SMART: SMO018: KRINGE.			
DR	SMART: SMO0130: KR_4.			
DR	SMART: SMO0473: PAN_AP_1.			
DR	SMART: SMO0020: TRYP-SGC_1.			
DR	PROSITE: PS00021: KRINGLE_1.			
DR	PROSITE: PS50070: KRINGLE_2.			
DR	Hydrolase, Serine protease.			
QO	Sequence_648 AA: 72781 MW: 4CSD70757350EA63 CRC64:			

```

Query Match Score 83: DB 4: Length 648:
Best Local Similarity 55.2%: Prod No. 3.1e-05:
Matches 12: Conservative 7: Mismatches 4: Indels 0: Gaps 0
OY 2 OGRHFCGALIHAFVPTASCF 24
||:|||||: :|||:|:|
DB 454 OGRHFCGSLVKEQMLTNAQCF 476

```

RESULT	15
014870	
ID	014870
AC	014870: PRELIMINARY: PRT: 711 AA.
DT	01-NOV-1996 (TREMBL: 01, Created)
ET	01-NOV-1996 (TREMBL: 01, Last sequence update)
OT	01-NOV-1991 (TREMBL: 01, Last annotation update)
DP	MACROPHAGE STIMULATING PROTEIN PRECURSOR.
CH	MS11
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_Taxid:9606:
UN	[1]
NP	SEQUENCE FROM N.A.
RC	TISSUE=LIVER.
EA	MEDLINE=93101411: PubMed-8193443:
RT	Cloning, sequencing, and expression of human macrophage stimulating
RT	protein (MSP, MS11) confirms MSP as a member of the family of kringle
RT	proteins and locates the MSP gene on chromosome 3.*;
RL	J. Biol. Chem. 268:15461-15468 (1993).
CC	-1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
CC	-1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR	EMBL: L11924; AA55872.1: "
DR	HSSP: P00747; 2P4.

FT NON TER 117 117
SO SEQUENCE 117 AA: 13038 MW: 37052EB7132BC56 CRC64;

Query Match 61.6%; Score 85; DB 13; Length 117;
Best Local Similarity 52.0%; Fred. No. 2.9e-06;
Matches 13; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY 1 NCGHRCGALIHARFWTASCRQ 25
DB 38 NCGHRCGSLVWAMVSAHCY 62

RESULT 8

042608 PRELIMINARY; PRT: 247 AA.
ID 042608
AC 042608
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TRYPsinogen A3 PRECURSOR.
GN TRYPsin.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Heterostei; Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN (1)
RP SEQUENCE FROM N.A.
RA Roach J.C.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RF PubMed: 18601254; trypsin.
RC TISSUE=ANTERIOR INTESTINE;
RA Roach J.C.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPsin FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: AF011899; AAB6955.1;
DR EMBL: AF011352; AAB5411.1;
DR HSP: P00763; IOP0.
DR MESOP: S011511;
DR INTERP: IPR001314; Chymotrypsin.
DR INTERP: IPR001254; trypsin.
DR Pfam: PF00089; trypsin.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPEC. 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyse: Serine protease; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 247 TRYPsin A3.
SO SEQUENCE 247 AA: 26295 MW: BCB03069A071DCB CRC64;

Query Match

Best Local Similarity 61.6%; Score 85; DB 13; Length 247;
Best Local Similarity 56.0%; Fred. No. 5.9e-06;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 NCGHRCGALIHARFWTASCRQ 25
DB 42 NCGHRCGSLVWAMVSAHCY 66

RESULT 9

042158 PRELIMINARY; PRT: 247 AA.
ID 042158
AC 042158
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE TRYPsinogen A2 PRECURSOR.
GN TRYPsin.
OS Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Heterostei; Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN (1)
RP SEQUENCE FROM N.A.
RA Roach J.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPsin FAMILY.
CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).
DR EMBL: AF011899; AAB6954.1;
DR HSP: P00760; IAO7.
DR INTERP: IPR001314; Chymotrypsin.
DR INTERP: IPR001254; trypsin.
DR Pfam: PF00089; trypsin.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPEC. 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyse: Serine protease; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 247 TRYPsin A2.
SO SEQUENCE 247 AA: AD3EB853197034 CRC64;

Query Match 61.6%; Score 85; DB 13; Length 247;
Best Local Similarity 56.0%; Fred. No. 5.9e-06;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 NCGHRCGALIHARFWTASCRQ 25
DB 42 NCGHRCGSLVWAMVSAHCY 66

RESULT 10

09077 PRELIMINARY; PRT: 247 AA.
ID 09077
AC 09077
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE 221010COTRIK PROTEIN.
DR EMBL: AF011899; AAB6955.1;
DR HSP: P00763; IOP0.
DR MESOP: S011511;
DR INTERP: IPR001314; Chymotrypsin.
DR INTERP: IPR001254; trypsin.
DR Pfam: PF00089; trypsin.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPEC. 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyse: Serine protease; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 247 TRYPsin A3.
SO SEQUENCE 247 AA: AD3EB853197034 CRC64;

Query Match

Best Local Similarity 61.6%; Score 85; DB 13; Length 247;
Best Local Similarity 56.0%; Fred. No. 5.9e-06;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 NCGHRCGALIHARFWTASCRQ 25
DB 42 NCGHRCGSLVWAMVSAHCY 66

RESULT 10

09077 PRELIMINARY; PRT: 247 AA.
ID 09077
AC 09077
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE 221010COTRIK PROTEIN.
DR EMBL: AF011899; AAB6955.1;
DR HSP: P00763; IOP0.
DR MESOP: S011511;
DR INTERP: IPR001314; Chymotrypsin.
DR INTERP: IPR001254; trypsin.
DR Pfam: PF00089; trypsin.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPEC. 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyse: Serine protease; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 247 TRYPsin A3.
SO SEQUENCE 247 AA: AD3EB853197034 CRC64;

Query Match

Best Local Similarity 61.6%; Score 85; DB 13; Length 247;
Best Local Similarity 56.0%; Fred. No. 5.9e-06;
Matches 14; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 1 NCGHRCGALIHARFWTASCRQ 25
DB 42 NCGHRCGSLVWAMVSAHCY 66

RESULT 10

09077 PRELIMINARY; PRT: 247 AA.
ID 09077
AC 09077
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE 221010COTRIK PROTEIN.
DR EMBL: AF011899; AAB6955.1;
DR HSP: P00763; IOP0.
DR MESOP: S011511;
DR INTERP: IPR001314; Chymotrypsin.
DR INTERP: IPR001254; trypsin.
DR Pfam: PF00089; trypsin.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPEC. 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyse: Serine protease; Signal.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 16 247 TRYPsin A3.
SO SEQUENCE 247 AA: AD3EB853197034 CRC64;

RESULT 2

061096 PRELIMINARY: PRT: 254 AA.

AC 061096 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 11, Last sequence update)

DT 01-AUG-1999 (TREMBLrel. 17, Last annotation update)

DE 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE PROTEINASE-3 (PROTEINASE 3) (FBI-PRO-PROTEINASE 3).

GN PRN3.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

XX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129SVJ;

RA Sturrock A., Franklin K.F., Wu S.Q., Hoidal J.R.;

RT "Characterization and localization of the genes for mouse proteinase-3 and neutrophil elastase.";

RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.

RM 3

RP SEQUENCE OF 2-254 FROM N.A.

RC STRAIN=BA1B/C;

RA MEDLINE-97362044; PubMed-92117433;

RT Aveskog M., Lutzelschab C., Huang M.R., Hellman L.;

RT "Characterization of cDNA clones encoding mouse proteinase 3 (myeloblastin) and cathepsin G.";

RL Immunogenetics 46:181-191(1997).

CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

DR EMBL: AF082186; AAC9701.1.

DR EMBL: U43535; AAB67271.1.

DR HSSP: P20160; IAB3.

DR MEROPS: S01.134; .

DR MGD: MGI:893580; Pten3.

DR InterPro: IP8001314; Chymotrypsin.

DR InterPro: IP8001324; Trypsin.

DR Pfam: PF00089; trypsin.1.

DR PRINTS: PR00723; CHYMOTRPSIN.

DR SMART: SM00134; TRYPSIN_HIS.

DR PROSITE: PS00135; TRYPSIN_SERP.1.

KW Hydrolyase; Protease; Serine protease.

SO SEQUENCE 254 AA; 27626 MW; 00CEB989A3CB79CA CRC64;

Query Match 71.0%; Score 98; DB 11; Length 254;

Best Local Similarity 73.9%; Pred. No. 4,7e-08;

Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

0Y 3 GNRHGGCALIHARVPTAASCP 35

DB 54 GSHRCGTLIHPSVFLAAHCLR 76

RESULT 3

09GME1 PRELIMINARY: PRT: 258 AA.

AC 09GME1

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=9258;

XX [1]

RP SEQUENCE FROM N.A.

RA Poorafshar M.M., Hellman L.L.;

RT "Identification and structural analysis of three serine proteases in a monotreme, platypus, Ornithorhynchus anatinus.";

RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.

CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

DR EMBL: AF275652; AAG00451.1.

DR InterPro: IP8001314; Chymotrypsin.

DR InterPro: IP8001324; Trypsin.

DR Pfam: PF00089; trypsin.1.

DR PRINTS: PR00723; CHYMOTRPSIN.

DR SMART: SM00134; TRYPSIN_HIS.

DR PROSITE: PS00134; TRYPSIN_SERP.1.

KW Hydrolyase; Serine protease.

SO SEQUENCE 258 AA; 28165 MW; 2E1732C300A36138 CRC64;

Query Match 71.0%; Score 98; DB 6; Length 258;

Best Local Similarity 73.9%; Pred. No. 4.8e-08;

Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

0Y 1 NGRHGGCALIHARVPTAASCP 23

DB 43 NGRHGGCALIHARVPTAASCP 65

RESULT 4

09U0D8 PRELIMINARY: PRT: 200 AA.

AC 09U0D8

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE PROTEINASE 3 (PROTEINASE 3) (FBI-PRO-PROTEINASE 3).

GN Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

XX [1]

RP SEQUENCE FROM N.A.

RA Clave E., Moldrem J., Hensel N., Rapels A., Barrett A.J.;

RT "Donor-recipient polymorphism of the proteinase 3 gene: A potential target for cellular immunoresponses to myeloid leukemia.";

RL Immunogenetics 46:181-191(1997).

CC -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.

CC -1- SIMILARITY: TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (S1).

DR EMBL: AF015449; AAD21524.1.

DR EMBL: AF015446; AAD21524.1; JOINED.

DR EMBL: AF015447; AAD21524.1; JOINED.

DR EMBL: AF015448; AAD21524.1; JOINED.

DR HSSP: P24158; IFUJ.

DR InterPro: IP8001314; Chymotrypsin.

DR InterPro: IP8001324; Trypsin.

DR Pfam: PF00089; trypsin.1.

DR SMART: SM00134; TRYPSIN_HIS.

DR PROSITE: PS00134; TRYPSIN_SERP.1.

KW Hydrolyase; Serine protease.

FT NON-TER 200

SO SEQUENCE 200 AA; 21609 MW; 13F35081D0E160A8 CRC64;

Query Match 67.4%; Score 93; DB 4; Length 200;

Best Local Similarity 64.0%; Pred. No. 2.4e-07;

Matches 16; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

0Y 1 NGRHGGCALIHARVPTAASCP 25

DB 50 NGRHGGCALIHPSVFLAAHCLR 74

RESULT 5

09DB10 PRELIMINARY: PRT: 799 AA.

AC 09DB10

DT 01-JUN-2001 (TREMBLrel. 17, Created)

Fri Apr 5 15:13:01 2002

us-09-657-276-1032.rsp

Page 12

OY 1 NOGHRFCGALIHARFVMTASCFQ 25
DB 44 NSGYRRCGSLISSOWYLSAARCYK 68

Search completed: April 5, 2002, 15:01:12
Job time: 106 sec

Query Match 60.1% Score 84: DB 1: Length 247;
Best Local Similarity 56.0%: Pred. No. 3.9e-06;
Matches 14: Conservative 7: Mismatches 4: Indels 0: Gaps 0:

OY 1 N0GRRFGCALIHARFVMTASCP0 25
DB 42 NAGYHRCGSLINOVVSAHCK0 66

RESULT 12
TRY2_XENLA STANDARD: PRT: 244 AA.

AC P70059:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE TRYPsin PRECURSOR (EC 3.4.21.4)

OS Xenopus laevis (African clawed frog)

OC Chordata: Vertebrata: Vertebrata: Euteleostomi:

OC Amphibia: Batrachia: Anura: Mesobatrachia: Pipiloidea: Pipilidae:

OC Xenopodinae: Xenopus.

OX NCBI_TaxID=8355;

RM (1)

RP SEQUENCE FROM N.A.

RA Wang K., Lytle L., Gan L., Hood L.E.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPsin FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL: U72330; AB01724.1; -

DR HSSP: P00763; 10PO.

DR MESOS: S01131; 10PO.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR001254; Trypsin.

DR Pfam: PF00089; trypsin.1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR SMART: SM00020; TRYP-SPEC.1.

DR PROSITE: PS00240; TRYPsin_DOM: 1.

DR PROSITE: PS00134; TRYPsin_HIS: 1.
DR PROSITE: PS00135; TRYPsin_SER: 1.
KM Hydrolase: Serine protease: Digestion: Zymogen: Signal:
KW Multigene family.
FT PROPEP 1 15
FT CHAIN 16 21
FT ACT_SITE 22 244
FT ACT_SITE 61 61
FT ACT_SITE 105 105
FT ACT_SITE 198 198
FT DISULFID 28 158
FT DISULFID 46 62
FT DISULFID 130 231
FT DISULFID 137 204
FT DISULFID 169 183
FT DISULFID 183 183
FT DISULFID 192 192
SO SEQUENCE 244 AA: 26079 MW: C63P29C83100B33 CRC64;

Query Match 60.1% Score 83: DB 1: Length 244;
Best Local Similarity 52.0%: Pred. No. 5.6e-06;
Matches 13: Conservative 5: Mismatches 3: Indels 0: Gaps 0:

OY 1 N0GRRFGCALIHARFVMTASCP0 25
DB 40 NAGYHRCGSLINOVVSAHCK0 64

RESULT 13
TRY3_RAT STANDARD: PRT: 247 AA.

AC P08426:

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE TRYPsin III, CATIONIC PRECURSOR (EC 3.4.21.4) (PRETRYPsinogen III).

OS Rattus norvegicus (Rat).

OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:

OC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.

OX NCBI_TaxID=10116;

RM SEQUENCE FROM N.A.

RA Fletcher T.S., Alhadeff M., Craik C.S., Larmann C.;

RL MEDLINE=67271609; PubMed=3607011;

RT Isolation and characterization of a cDNA encoding rat cationic

RT trypsinogen.

CC -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-

CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE

CC TRYPsin FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL: M16624; AAA1985.1; -

DR PIR: A27547; A27547.

DR HSSP: P00763; 10PO.

DR MESOS: S01131; 10PO.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR001254; Trypsin.

DR Pfam: PF00089; trypsin.1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR SMART: SM00020; TRYP-SPEC.1.

DR PROSITE: PS00240; TRYPsin_DOM: 1.

DR PROSITE: PS00134; TRYPsin_HIS: 1.
DR PROSITE: PS00135; TRYPsin_SER: 1.
KM Hydrolase: Serine protease: Digestion: Zymogen: Signal:
KW Multigene family.
FT PROPEP 1 15
FT CHAIN 16 24
FT ACT_SITE 25 247
FT ACT_SITE 64 64
FT ACT_SITE 108 108
FT ACT_SITE 201 201
FT DISULFID 31 161
FT DISULFID 49 65
FT DISULFID 133 234
FT DISULFID 140 207
FT DISULFID 172 186
FT DISULFID 186 186
FT DISULFID 195 195
SO SEQUENCE 247 AA: 26459 MW: D74892AA5848A8 CRC64;

Query Match 60.1% Score 83: DB 1: Length 247;
Best Local Similarity 52.0%: Pred. No. 5.7e-06;
Matches 13: Conservative 9: Mismatches 3: Indels 0: Gaps 0:

OY 1 N0GRRFGCALIHARFVMTASCP0 25

Query Match	61.8%	Score 85:	DB 1:	length 248:
Best Local Similarity	52.0%	Pred.	2.8e-06:	
Matches 13:	Conservative	9:	Mismatches 3:	Indels 0:
			Gaps	0:
DB	44	1	NOGRRPGGALIHARFVATASCRQ	25
		1	: : :	68
			44	NSGTRPGGSLNSQVLSANACRTR

FT	PROPER	24	25	ACTIVATION PERTIOD.
FT	CHAIN	26	258	GRANZYME K.
FT	ACT_SITE	66	66	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	110	110	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	208	208	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	DISULFID	51	67	BY SIMILARITY.
FT	DISULFID	153	74	BY SIMILARITY.
FT	DISULFID	173	173	BY SIMILARITY.
FT	DISULFID	204	228	BY SIMILARITY.
5Q	SEQUENCE	258 AA;	28465 MW;	988A071D09B8AFB84 CRC64;

Query Match	Score 85;	DB 1;	Length 258;
Best Local Similarity	56.5%;	Pred. No. 2,96-06;	
Matches 13;	Conservative	6;	Mismatches 4;
			Indels 0;
			Gaps 0;

QY	2	QGRHGGALGTHAPVTAASCF	24
		: : : : : : : : : : : : : : : : :	
Db	46	RGNHCGVLTIRPQWVLTAAHAC	68

RESULT	6	STANDARD:	PRT: 258 AA.
ID	GRAK_RAT		
CD	PA9864:		
DT	01-OCT-1996 (rel. 34, Last sequence update)		
DT	01-OCT-1996 (rel. 34, Last sequence update)		
DT	30-MAY-2000 (rel. 39, Last annotation update)		
DE	GRAMININ, K PRECURSOR (EC 3.4.21.-) (NK-TRYPTASE-2) (NK-TRYP-2),		
GN	GMAK.		
OS	Rattus norvegicus (Rat).		
OS	Mus musculus, Metacoel, Chordata; Canitales; Vertebrata; Euteleostomi;		
OX	Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCHL_TextID=10116;		
RP	SEQUENCE FROM N.A.A. AND SEQUENCE OF 26-58.		
RX	STRAIN=FISCHER 344; TISSUE=Lymphocytes;		
RX	MEDLINE=94179809; Pubmed=8133042;		
RA	Snyder T.J., Miltout T.A., Smyth M.J., Ottaway K.S., Pillaro A.M.,		
RA	Sawyer R., Henderson L.E., Spengler H., Lloyd A.R.;		
RT	"Purification and cloning of a novel serine protease, RAK-Tryp-2,		
RT	from the granules of a rat NK cell leukemia."		
RL	J. Immunol. 152:2289-2297(1994).		
CC	-1- SUBCELLULAR LOCATION: CYTOSOLIC GRANULES.		
CC	-1- TISSUE SPECIFICITY: SPLEEN, LUNGS AND LIVER NONPARANEURAL CELLS.		
CC	-1- SIMILARITY: BELONGS TO PERIDASE FAMILY S1; ALSO KNOWN AS THE		
CC	PERLIN FAMILY; STRONGEST TO OTHER GRAMININS AND TO MAST CELL		
CC	PROTEASES.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation.		
CC	CC The European Bioinformatics Institute. There are no restrictions on ways		
CC	CC use by non-profit institutions as long as its content is in no way		
CC	CC modified and this statement is not removed. Usage by and for commercial		
CC	CC entities requires a license agreement (see http://www.ebi.ac.uk/submit/announce/		
CC	or send an email to license@ebi.ac.uk).		
CC	-----		
DR	EMBL: L15694; AAA2057.1; -		
DR	HSSP: P00761; IDPO.		
DR	NCBI: S011485; S011485.		
DR	InterPro: IPR001334; TRYPSP1n.		
DR	InterPro: IPR001254; TRYPSP1n.		
DR	Pfam: PF00089; trypsin.1		
DR	PRINTS: PR00722; CHW0RFP1n.		
DR	SMART: SM00020; TRYP_SFC.1.		
DR	PROSITE: PS50240; TRYPSP1_DOM.1.		
DR	PROSITE: PS00134; TRYPSP1_HIS.1.		
DR	PROSITE: PS00135; TRYPSP1_SER.1.		
DR	HYDROLASE; Serine protease; zymogen; Signal.		
DR	SIGNAL		
DR	1		
DR	23		
DR	POTENTIAL.		

CC PS0142: .
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MAST CELL TRYPTASE PRECURSOR (EC 3.4.21.59).
OS Melones unguliculatus (Mongolian jird).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meliones.
CX NCBI_TaxID=10047.
NM (1)
NM SEQUENCE FROM N.A.
NM STRAIN=MG5/SE2, TISSUE=Intestine;
NM Murakami Y, Osada I, Fukuda S, 1997,11;
NM Murakami Y, Borrelli V, Itoh N, Tomita M., Kobayashi T.,
NM Maruyama H., Borrelli V, Itoh N, Murakami Y, 1997,11;
RT "Cloning of the cDNA encoding mast cell tryptase of
RT Meliones unguliculatus, and its preferential expression in the
RT Intestinal mucosa".
RL Biochem. J. 309: 921-926 (1995).
CC -1- CATALYTIC ACTIVITY: PREPREFERENTIAL CLEAVAGE: ARG-1-, LYS-1-, BUT
CC WITH MORE RESTRICTED SPECIFICITY THAN TRYPSIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY. STRONGEST TO OTHER TRYPSASES.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use, but the EMBL outstation must be acknowledged in any publication.
CC modified and this statement must be removed and replaced by "reformatted
CC CC entries requires a license agreement (see <http://www.1ab-stb.ch/announce/>;
CC or send an email to license@1ab-stb.ch)".
CC
DR EMBL: D31789; BA06598.1; .
DR HSSP: P20231; IMO.
DR MEROPS: S01.143;
DR InterPro: IPR001314; C1YMOTrypsin.
DR InterPro: IPR001254; Trypsin.
DR Pfam: PF00089; trypsin.1.
DR Pfam: PF00092; CatMOTrypsin.
DR DRIPAT: S00072; Trypsin.DMS.1.
DR DR PROSITE: PS00140; TRYPSIN_DOM. 1.
DR PROSITE: PS00134; TRYPSIN_HIS. 1.
DR PROSITE: PS00135; TRYPSIN_SSR. 1.
KW Hydrolase; Serine protease; signal; Glycoprotein.
FT SIGNAL 1
FT CHAIN 26 .. 270
FT ACT_SITE 69 69 69
FT ACT_SITE 116 116 116
FT
FT POTENTIAL 1
FT MAST CELL TRYPTASE.
FT CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 116 116 116

RX	MEDLINE-90332035; PubMed237728
RA	Jenne D.E., Tachop J., Luedemann J., Utecht B., Gross W.L.;
RT	"Megener's autoantigen decoded";
RM	Nature 346:520-520(1990).
RM	[10]
RT	IDENTITY OF MEGENER'S AUTOANTIGEN WITH PROTEINASE 3;
RA	Re P, Rost G, Kasperk H, Schmid C, Niles J, R.T., Arnaut M.A.;
RT	Gupta S.R. (1992) "Identity of Megener's autoantigen (p29) with Proteinase 3 and
RT	myeloblastin";
RM	Blood 76:2162-2162(1990).
RM	[11]
RN	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RA	MEDLINE-96346178; PubMed8757293;
RA	Fujisawa M., Charnatal M.M., Halenbeck R., Roths K., James M.N.G.;
RT	"The crystal structure of PR3, a neutrophil serine proteinase antigen
CC	of Megener's glomerulonephritis antibodies";
CC	-1- FUNCTION: POLYMORPHONUCLEAR LEUKOCYTE SERINE PROTEASE THAT
CC	DERADES ELASTIN, FIBRONECTIN, LAMININ, VITROECTIN AND COLLAGEN
CC	TYPES I, II, AND IV (IN vitro). INSUPATION TO HAMSTERS.
CC	-1- CATALYTIC ACTIVITY: HYDROLYSIS OF PROTEINS, INCLUDING ELASTIN, BY
CC	PREFERENTIAL CLEAVAGE: ALA- -XAA > VAL- -XAA.
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY 51; ALSO KNOWN AS THE
CC	TRYPsin FAMILY, ELASTASE SUBFAMILY.
CC	--
CC	This SwissProt entry is copyright. It is produced through a collaboration
CC	between the Swiss Biotechinformatics Institute and the Bioinformatics
CC	Centre at the European Bioinformatics Institute. These two organisations are
CC	used by non-profit institutions insofar as their products are made available
CC	as modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.ebi.ac.uk/comm/usage/
CC	or send an email to license@ebi.ac.uk).
CC	--
DR	EMBL; X56137; CAJ93598.1;
DR	EMBL; M505479; AAB54988.1;
DR	EMBL; M56839; AAB59493.1;
DR	EMBL; M56839; AAB59493.1; JOINED.
DR	EMBL; M56837; AAB59493.1; JOINED.
DR	EMBL; X55668; CAJ93203.1;
DR	EMBL; M29142; AAA63412.1;
DR	EMBL; M96628; AAB59364.1;
DR	PIR; AA3983; PRHU3.
DR	PDB; 1FDU; 1J-JUL-96.
DR	KM00337020.134; -.
DR	InterPro: IPRO01314; ChymoTrypsin.
DR	InterPro: IPRO01254; Trypsin.
DR	Pfam: PF00089; trypsin.1.
DR	PRINTS; PR00722; CHYMOTRYPsin.
DR	SMART; SM00020; TRYp-SPEC.
DR	PROSITE; PSS00340; TRYPsin_DOM_1.
DR	PROSITE; PS00134; TRYPsin_HIS_1.
DR	PROSITE; PS00135; TRYPsin_SER_1.
KW	3D-structure.
FT	SIGNAL. 1 25
FT	PROPEP. 26 27
FT	CHAIN. 28 248
FT	PROPEP. 249 256
FT	ACT_SITE. 71 71
FT	ACT_SITE. 118 118
FT	CATALytic SITE. 203 209
FT	CARBOND. 129 129
FT	CARBOND. 139 139
FT	DISULFID. 56 72
FT	DISULFID. 152 209
FT	DISULFID. 182 188
FT	DISULFID. 199 224
FT	CONFLICT. 2 2
FT	CONFLICT. 46 46
O -> R (IN REF. 3).	
O -> E (IN REF. 8).	
CHARGE RELAY SYSTEM.	
CHARGE RELAY SYSTEM.	
CHARGE RELAY SYSTEM.	
N-LINKED (GLCNAC. . .) (POTENTIAL).	
N-LINKED (GLCNAC. . .).	
MYELOBLASTIN.	

```

FT CONFLICT      64      64      S -> D (IN REF. 5).
PT CONFLICT      70      70      A -> P (IN REF. 1).
TT CONFLICT     119     119      V -> I (IN REF. 1 AND 5).
CT CONFLICT     135     136      A -> TS (IN REF. 1 AND 5).
PT CONFLICT     255     255      MISSING (IN REF. 3).
S0 SEQUENCE      256 AA: 27807 MW: CBCCA36D8CB42A40 CRC64:

Query Match          67.4%   Score 93: DP 1: Length 256:
Best Local Similarity 64.0%   Pred. No. 1:6e-07:
Matches 16: Conservative 2: Mismatches 7: Indels 0: Gaps 0:

Db      1 NCORHPCGALLIHARVWTFMAASCP 25
        | | | | | | | | | | | | | | :
        50 NPGSHPCGOTLIRHSFVLTMACLR 74

RESULT  4
TYPE: PIC
ID       TRYP_PIC              STANDARD:             PRT:    231 AA.
AC       P00761:
DT       21-JUL-1986 (rel. 01, Created)
DT       21-JUL-1986 (rel. 01, Last sequence update)
DT       15-DEC-1998 (rel. 37, Last annotation update)
DE       TRYPSIN PRECURSOR (EC 3.4.21.4).
OS       Sus scrofa (Pig).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CM       Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
LN       MCL1_Taxid=9833:
RA       Sequence of 1-10.
RP       Charles M., Rovery M., Guidoni A.A., Desnuelle P.:
RT       "On trypsinogen and trypsin of Pig".
RL       Blochim. Biophys. Acta 69:115-129(1963).
LN       [2]
SEQUENCE OF 9-231.
RX       MEDLINE=97328692: PubMed=4738933:
RA       Hermanson M.R., Ericsson L.H., Neurath H., Walsh K.A.:
RT       Determination of the amino acid sequence of porcine trypsin by
RL       biochemical methods. J Biol Chem 247:1117-1121(1972).
LN       [3]
RX       X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RA       Huang Q., Liu S., Tang Y., Zeng F., Qian R.:
RT       Refined 1.6-A resolution crystal structure of the complex formed
RT       between porcine beta-trypsin and MCLT-A, a trypsin inhibitor of the
RT       squam family. Detailed comparison with bovine beta-trypsin and its
RT       complex. Biol. 229:1022-1030(1993).
LN       [4]
RX       X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RA       MEDLINE=97201369: PubMed=1551419:
RT       Huang Q., Liu S., Tang Y., Zeng F., Qian R.:
RT       Amino acid sequencing of a trypsin inhibitor by refined 1.6 A x-ray
RT       crystal structure of a complex with porcine beta-trypsin. J.
RT       FEBS Lett. 297:143-146(1992).
LN       [5]
RX       X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RA       MEDLINE=95030507: PubMed=7943985:
RT       Huang Q., Wang Z., Li Y., Liu S., Tang Y.:
RT       Refined 1.8-A resolution crystal structure of the porcine epsilon-
RT       trypsin. Biophys. Acta 1209:77-82(1994).
LN       [6]
RX       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) IN COMPLEX WITH LGFL.
RA       MEDLINE=97330427: PubMed=924286:
RT       Hubner R., Pfelebecker R.K., Sturtebchner J., Bauer M., Bode W.,
RT       Hubner R., Pfelebecker R.K., Sturtebchner J., Bauer M., Bode W.,
RT       Hubner R., Pfelebecker R.K., Sturtebchner J., Bauer M., Bode W.,
RT       Thierwald E.A.:
RT       The three-dimensional structure of recombinant leech-derived
RT       trypsinase inhibitor in complex with trypsin. Implications for the
RT       structure of human mast cell trypsinase and its inhibition. J.

```

RT antibacterial and monocyte-specific chemotactic glycoprotein
RA structurally similar to neutrophil elastase.*
RL FEBS Lett. 272:200-204(1990).
RN (6)
RN SEQUENCE OF 27-248.
RP MEDLINE-9209157. Published-2026172.
RX Fildgaard H., Oestergaard E., Ingene S., Svendsen A., Thomsen J.,
RA Engels M., Wollmer A.,
RA Fildgaard H., Oestergaard E., Ingene S., Svendsen A., Thomsen J.,
RT "PNA elastases: a comparison of the specificity of human lysosome
RT the enzyme from other species on different substrates and inhibitors.*"
RL Arch. Biochem. Biophys. 286:284-292(1993).
RN (8)
RN SEQUENCE OF 27-46.
RP MEDLINE-8931847. Published-2501794.
RX Morris M.N., Seeger M.W., Campanelli D., Griffith J., Wilde C.,
RA Morris M.N., Seeger M.W., Campanelli D., Griffith J., Wilde C.,
RT "Antibiotic proteins of human polymorphonuclear leukocytes.*"
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
RN (9)
RN SEQUENCE OF 27-46 AND 194-217.
RX MEDLINE-9013040. Published-2404973.
RA Wilde C.G., Sable J.L., Griffith J.E., Scott R.W.,
RT "Characterization of two azurophilic granule proteases with active-site
RT homology to neutrophil elastase.*"
RL J Biol. Chem. 265:2038-2041(1990).
RN (10)
RN SEQUENCE OF 27-67.
RP TISSUE-Neutrophilia:
RX MEDLINE-90157837. Published-2406577.
RA Perrella H.A., Spitznagel J.K., Pohl J., Wilson D.E., Morgan J.,
RT Polling I., Larrick J.W.,
RA "CAP 37, a 37 kd human neutrophilic granule cationic protein shares
RT homology with inflammatory proteinases.*"
RL Life Sci. 46:189-196(1990).
RN (11)
RN SEQUENCE OF 27-69.
RP TISSUE-Neutrophilia:
RX MEDLINE-90237224. Published-2332603.
RA Perrella H.A., Shaffer W.M., Pohl J., Martin L.E., Spitznagel J.K.,
RT "CAP37, a human neutrophilic protein is a chemotactic factor with monocyte
RT specific activity.*"
RL J. Clin. Invest. 85:1468-1476(1990).
RN (12)
RN REVIEW.
RP MEDLINE-9209171. Published-1753533.
RX Morgan J.G., Perrella H.A., Sukienicki T., Spitznagel J.K.,
RA "Human neutrophilic granule cationic protein CAP37 is a specific
RT macrophage chemotaxin that shares homology with inflammatory
RT proteinases.*"
RL Adv. Exp. Med. Biol. 305:89-96(1991).
RN (13)
RN SYNTHESIS OF 46-70.
RP MEDLINE-93281653. Published-8506327.
RX Perrella H.A., Erdem I., Pohl J., Spitznagel J.K.,
RA Perrella H.A., Erdem I., Pohl J., Spitznagel J.K.,
RT "A 37 kDa human neutrophilic granule cationic protein
RT chemotactic for monocytes.*"
RL Proc. Natl. Acad. Sci. U.S.A. 90:4733-4737(1993).
RN (14)
RN X-RAY CRYSTALLOGRAPHY (2.3 Å RESOLUTIONS).
RP MEDLINE-97249288. Published-9095193.

3A	Iversen L.F., Kastrop J.S., Bjoern S.E., Rasmussen P.B., Moeberg P.C., Ploeggaard L.F., Larsen I.K.;	100.0%	Score 198;	DB 1;	Length 281;
3B	Structure of Hsp a multifunctional protein with a serine proteinase fold.;				
3C	Nat. Struct. Biol. 4:265-268(1997).				
3D	X-RAY CRYSTALLOGRAPHY (1.12 ANGSTROMS).				
3E	Katelson S., Iversen L.P., Larsen I.K., Ploeggaard H.J., Kastrop J.S.;				
3F	Atomic resolution structure of human HBP/Ca37/zincocidin.;				
3G	Acta Crystallogr. D 54:588-609(1998).				
3H	-1- FUNCTION: THIS IS A NEUTROPHIL GRANULE-DERIVED ANTIBACTERIAL AND MONOCYTE- AND FIBROBLAST-SPECIFIC CHEMOTACTIC GLYCOPROTEIN. BINDS HEPARIN. THE CYTOTOXIC ACTION IS LIMITED TO MANY SPECIES OF GRAM-NEGATIVE BACTERIA. THIS SPECIFICITY MAY BE EXPLAINED BY A STRONG AFFINITY OF THE VERY BASIC N-TERMINAL HALF FOR THE NEGATIVELY CHARGED LIPIDOLISACCHARIDES THAT ARE UNIQUE TO THE GRAM-NEGATIVE CELL WALL. THIS PROTEIN MAY ALSO PLAY A ROLE IN MEDIATING RECRUITMENT OF MONOCYTES TO THE SECOND WAVE OF INFLAMMATION.				
3I	-1- SUBUNIT: MONOMER.				
3J	-1- SIMILARITY: BELONGS TO CYTOSOLIC GRANULES OF NEUTROPHILS. TRYPsin FAMILY. ELASTASE SUBFAMILY.				
3K	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in European Bioinformatics Institute. There are no restrictions on its use. The copyright for this entry is held by the EMBL Outstation in the UK. modified and this statement is not removed by those who use it and for commercial entities requires a license agreement (see http://www.1ab.sib.ch/announc/c/ or send an email to license@1ab.sib.ch).				
3L	EMBL; M96326; AAB59333.1;				
3M	EMBL; X58794; CAA11601.1;				
3N	EMBL; AC004799; AAC18957.1;				
3O	PIR; A46435; TRBUZ2.				
3P	PDB; 1AE256; 1AE256.				
3Q	PDB; 1A75; 2J-MAR-99.				
3R	MEROPS: S01.971.				
3S	MIM: 162815.				
3T	InterPro: IPR001314; Chymotrypsin.				
3U	InterPro: IPR001254; Trypsin.				
3V	Pfam: PF00089; trypsin.1.				
3W	PRINTS: PR00722; CHYMOTRYPSIN.				
3X	SMART: SM00020; TRYD-SPEC.1.				
3Y	PROSITE: PSS0014; TRYPsin_DOM. 1.				
3Z	PROSITE: PSS0135; TRYPsin_PHS. FALSE NEG.				
4A	Settle-Case 00135; TRYPsin_GEN. FALSE NEG.				
4B	Heparin-binding; Signal: 30 structure.				
4C	Signal				
4D	CHAIN				
4E	PROPEP				
4F	DOMAIN				
4G	CARBOHYD				
4H	CARBOHYD				
4I	CARBOHYD				
4J	DISULFID				
4K	DISULFID				
4L	DISULFID				
4M	DISULFID				
4N	DISULFID				
4O	DISULFID				
4P	DISULFID				
4Q	DISULFID				
4R	DISULFID				
4S	DISULFID				
4T	DISULFID				
4U	DISULFID				
4V	DISULFID				
4W	DISULFID				
4X	DISULFID				
4Y	DISULFID				
4Z	DISULFID				
5A	DISULFID				
5B	DISULFID				
5C	DISULFID				
5D	DISULFID				
5E	DISULFID				
5F	DISULFID				
5G	DISULFID				
5H	DISULFID				
5I	DISULFID				
5J	DISULFID				
5K	DISULFID				
5L	DISULFID				
5M	DISULFID				
5N	DISULFID				
5O	DISULFID				
5P	DISULFID				
5Q	DISULFID				
5R	DISULFID				
5S	DISULFID				
5T	DISULFID				
5U	DISULFID				
5V	DISULFID				
5W	DISULFID				
5X	DISULFID				
5Y	DISULFID				
5Z	DISULFID				
6A	DISULFID				
6B	DISULFID				
6C	DISULFID				
6D	DISULFID				
6E	DISULFID				
6F	DISULFID				
6G	DISULFID				
6H	DISULFID				
6I	DISULFID				
6J	DISULFID				
6K	DISULFID				
6L	DISULFID				

555067
 trypsin [EC 3.4.21.4] I precursor, pancreatic - chicken
 N:Altemate names: trypsinogen I
 C:Species: Gallus gallus (chicken)
 C:Specimen: 1997-01-19
 C:Accession: S55067, S72345, S55065, S72346, S71155
 R:Wang, K.; Gan, L.; Lee, I.; Hood, L.
 J. Biochem. J. 307, 471-479, 1995
 A:Title: Isolation and characterization of the chicken trypsinogen gene family.
 A:Reference number: S55065; MUID:95351611
 A:Accession: S55067
 A:Molecule type: DNA
 A:Residues: 1-748
 A:Cross-references: EMBL:U01516; NID:9603904
 A:Experimental source: clone 1-P38
 A:Accession type: S72345
 A:Molecule type: DNA
 A:Residues: 1-748 <MAN2>
 A:Experimental source: clone 1-P38
 A:Accession type: S72345
 A:Molecule type: mRNA
 A:Residues: 1-9, 'A', 11-12, 'T', 14-102, 'A', 104-214, 'T', 216-248 <MAN3>
 A:Cross-references: EMBL:U01515; NID:9603902; PIDs:AA79912.1; PTD:9603903
 A:Experimental source: clone P1
 A:Accession: S72346
 A:Molecule type: DNA
 A:Residues: 1-9, 'A', 11-12, 'T', 14-102, 'A', 104-214, 'T', 216-248 <MAN4>
 A:Cross-references: db:U01515; NID:9603902; PIDs:AA79912.1; PTD:9603903
 A:Experimental source: clone P1
 A:Accession: S71155
 A:Reference number: S71155
 submitted to the EMBL Data Library, September 1994
 A:Accession: S71155
 A:Molecule type: RNA
 A:Residues: 1-102, 'A', 104-248 <MAN5>
 A:Cross-references: EMBL:U01516; NID:9603904; PIDs:AA79913.1; PTD:9603905
 A:Experimental source: clone 1-P38
 A:Accession type: S71155
 A:Molecule type: RNA
 R:Keywords: hydrolysis, pancreas, protein digestion, serine proteinase, zymogen
 F:1-5/Domain: signal sequence, status predicted <SID>
 F:16-26/Domain: activation peptide, status predicted <APT>
 F:26-248/Product: trypsin I status predicted <MAT>
 F:26-249/Domain: trypsin homology <HTR>
 F:65-109/202/Active site: His, Asp, Ser status predicted

```
Query Match      Score 83; DB 2; Length 248;
Best Local Similarity 57.0%; Pred. No. 4,8e-05;
Matches 13; Conservative 8; Mismatches 4; Indels 0; Gaps 0.
```

Result 14
 macrophage-stimulating protein 1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 03-May-1994 (sequence, revision 14-Nov-1997 #text:Change 18-Jun-1999
 C:Accession: A40311; RefSeq: A41166; M61395
 Biochemistry 30, 9766-9769, 1991-97-8
 A:Title: Characterization of the DNPS12 locus on human chromosome 3: Identification of
 A:Reference number: A40311; MID:92002016

A:Accession: BA0331
A:Cross-references: GB:M74179
A:Molecule type: DNA
A:Residues: 1-711 <HA1>
A:Molecule type: DNA
A:Accession: BA0331
A:Cross-references: GB:M74179
A:Molecule type: mRNA

A:Residues: 1-111 <ER3>
 A:Cross-references: DB:M74178, NID:q183976, PDB:AAA506151, PDB:q183977
 A:Yoshimura, T., 268, 51661-51689, 1994; Steel, A.; Leonard, E.J.
 A>Title: Cloning, sequencing, and expression of human macrophage stimulating protein
 A:Reference number: M7136; NID:9340141
 A:Accession: M7136
 A:Molecule type: mRNA
 A:Residues: 1-12, 'C', 14-622, 'F', 624-711 <YOS>
 A:Cross-references: GB:111934; NID:q938017; PDB:AAA59872.1; PDB:q398018
 A:Notes: authors translated the codon tag for residue 623 as Leu; parts of this sequen
 R:Steel, A.; Yoshimura, T.; Shovelton, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
 R:Exp. Med. 173, 1227-1234, 1991; protein: purification, partial amino acid sequence, a
 A:Reference number: M61395; NID:91217655
 A:Accession: M61395
 A:Molecule type: Protein
 A:Residues: 230-247;288-291, 'E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310;326-
 A:Experimental source: Plasma
 C:Genetics:
 A:Gene: GDB:M571, D3P1552, DNF1552; HGFL
 A:Cross-references: GDB:128833; OMIM:142408
 A:Map position: 3p21-3p21.3 heterodimer of chaina derived from the same precursor
 C:Complex: Disulfide bond: growth factor: kringle homology: trypsin inhibitor
 C:Keywords: duplication; glycoprotein; growth factor; kringle; plasma
 F:1-19<ER3>: signal sequence status predicted <SIG>
 F:19-483,484-711<Prodnc>: macrophage-stimulating protein 1 statusa predicted <MA>
 F:110-187<Domain>: alpha chain statusa predicted <ACH>
 F:110-186<Domain>: kringle homology <KR1>
 F:191-268<Domain>: kringle homology <KR2>
 F:283-361<Domain>: kringle homology <KR3>
 F:370-448<Domain>: kringle homology <KR4>
 F:484-704<Domain>: beta chain statusa predicted <BCH>
 F:484-704<Domain>: trypsin homology <TR>
 F:55-78,60-186,111-169,137-181,131-328,212-251,240-263,283-361,304-343,332-355
 F:355-396,619<Binding site>: carbohydrate (asn) (covalent) statusa predicted

```

RESULT 15
A61345
    plasmin (EC 3.4.21.7) precursor - horse (fragments)
N:Alternate names: plasminogen
N:Contains: multiphasinogen
C:Species: Equus caballus (domestic horse)
C:Date: 28-Oct-1994 sequence_revision 01-Nov-1996 text_change 18-Jul-1997
C:Id: A61345 A61377

```

Enzyme 40, 63-69, 1988
 Brief structural aspects of the plasminogen of various species.
 A:Reference: 161545; M01D: 80050015
 A:Accession: A61545
 A:Molecule type: protein
 A:Residues: 1-33,34-117 <SCH>
 R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
 Protein Seq. Data Anal. 4, 69-74, 1991
 A>Title: Complete amino acid sequence of equine miniplasminogen.
 A:Accession: S17527; M01D: 92050074
 A:Molecule type: protein
 A:Residues: 118-455 <SCD>
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homol
 C:Keyword: fibrinolysis; glycoprotein; hydrolase; kringe; plasma; serine proteinase
 E:1-33,34-117,118-455/Product: plasminogen (trypsin) status experimental <pro>

R:Green, B.C.; Weston, H.; Ashe, B.M.; Doherty, J.; Finke, P.; Hagmann, W.; Lark, M.; M
Arch. Biochem. Biophys. 286, 284-292, 1991
A:Title: PMN elastases: a comparison of the specificity of human isoforms and the enzyme
A:Reference number: S14736; M01D:93178304
A:Accession: S14738
A:Keywords: trypsin; protein
A:Residues: 27-47 <CRP>
R:Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Marra, M.N.; Seeger
Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989
A:Title: Anticlotting proteins of human polymorphonuclear leukocytes.
A:Reference number: A33913; M01D:89315847
A:Accession: B33913
A:Molecule type: protein
A:Residues: 27-46 <GNB>
R:Peterson, H.A.; Shaffer, W.M.; Poh, J.; Martin, L.E.; Splitznagel, J.K.
J. Biol. Chem. 263, 166-176, 1988
A:Title: Cloning and characterization of a human neutrophil-derived chemocytic factor with monocyte specific act
A:Reference number: A60708; M01D:90373224
A:Accession: A60708
A:Molecule type: protein
A:Residues: 27-68 <PER>
R:Wasiuk, K.R.; Skubitz, K.M.; Gray, B.H.
Infect. Immun. 59, 4193-4200, 1991
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar
A:Reference number: A43600; M01D:93040097
A:Accession: B43600
A:Molecule type: protein
A:Residues: 27-48 <PMS>
R:Myasnik, K.T.; Bodreau, A.L.
Infect. Immun. 60, 4973-4975, 1992
A:Title: Human neutrophil azurocidin synergizes with leukocyte elastase and cathepsin G
A:Reference number: A49211; M01D:93014226
A:Accession: A49211
A:Molecule type: protein
A:Residues: 27-46 <MTV>
A:Note: sequence extracted from NC91 backbone (NCBIP:115511)
R:Sheppard, J.E.; Leitch, H.A.; Lojain, P.M.; McMaster, W.R.; Levy, J.G.
Exp. Hematol. 19, 138-142, 1991
A:Title: Characterization of two azurophil granule proteases with active-site homology b
A:Reference number: A43981; M01D:90130450
A:Accession: B43981
A:Molecule type: protein
A:Residues: 27-35, H, 37-46, 194-217 <MTD>
R:Peterson, H.A.; Shaffer, W.M.; Poh, J.; Martin, L.E.; Splitznagel, J.K.
Life Sci. 46, 169-176, 1990
A:Title: CAP 37 a 37 kD human neutrophil granule cationic protein shares homology with
A:Reference number: PH0081; M01D:93157837
A:Accession: PH0081
A:Molecule type: protein
A:Residues: 27-67 <PE2>
A:Experimental source: polymorphonuclear leukocyte
C:Comment: This protein is homologous to serine proteases but lacks proteolytic activi
lectrical activity against a number of gram-negative bacteria.
A:Accession: PH0081
A:Keywords: trypsin; inflammation
F:1-19/Domain: signal sequence \$status predicted <SIG>
F:20-26/Domain: amino-terminal propeptide \$status predicted <PRO>
F:27-248/Product: azurocidin \$status experimental <MAT>
F:27-239/Domain: trypsin homology <TRY>
F:67-115,201/Region: defective catalytic triad
F:249-251/Domain: carboxyl-terminal propeptide \$status predicted <CTP>

F:52-68/Disulfide bonds: \$status experimental
F:126-140,171/Binding site: carbohydrate (asn) (covalent) \$status experimental
F:149-207,180-186,197-222/Disulfide bonds: \$status predicted

Query Match 100.0% Score 138; DB 1; Length 231;
Best Local Similarity 100.0%; Pred. No. 3, 1e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NGRHFCGALIHARFVMTAASCPQ 25
|||||
DB 46 NGRHFCGALIHARFVMTAASCPQ 70

RESULT 2
TRYPsin - p19
N:Alternative names: heparin-binding protein
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 31-Mar-1992 \$sequence_revision 31-Mar-1992 \$text_change 18-Jul-1997
C:Accession: S15393
R:Pfodgaard, H.; Ostergaard, E.; Bayne, S.; Svendsen, A.; Thomsen, J.; Engels, M.; Wo
Eur. J. Biochem. 197, 535-547, 1991
A:Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of po
A:Reference number: S15393; M01D:91224149
A:Accession: S15393
A:Molecule type: protein
A:Residues: 1-219 <FPO>
R:Soerensen, H.H.; Thomsen, J.; Bayne, S.; Hojrup, P.; Roepstorff, P.
Biomol. Environ. Mass Spectrom. 19, 713-720, 1990
A:Title: Strategies for determination of disulfide bridges in proteins using plasma
A:Reference number: A37448; M01D:91167744
A:Contents: annotation; disulfide bonds
C:Superfamily: trypsin; trypsin homology
C:Keywords: glycoprotein
F:1-211/Domain: trypsin homology <TRY>
F:141,68,173/Region: defective catalytic triad
F:212-219,152-156/Disulfide bonds: \$status experimental
F:113/144/Binding site: carbohydrate (asn) (covalent) \$status experimental

Query Match 74.6% Score 103; DB 1; Length 219;
Best Local Similarity 75.0%; Pred. No. 4, 6e-08;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QGRHFCGALIHARFVMTAASCPQ 25
|||||
DB 21 QGRHFCGALIHARFVMTAASCPQ 44

RESULT 3
PREHII
A:Alternative names (EC 3.4.21.-) precursor [validated] - human
N:Alternative names: NG27; C-MNCA antigen; neutrophil proteinase 4; p29; Wegener's gran
N:Contents: myeloblastin
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1993 \$sequence_revision 31-Mar-1993 \$text_change 08-Dec-2000
C:Accession: A45080; B45268; A43983; J04031; A33751; S1091; A51176; A60148; A43982;
R:Sturrock, A.B.; Franklin, K.F.; Rao, G.; Marshall, B.C.; Rebenitsch, M.B.; Demons
J. Biol. Chem. 267, 21193-21197, 1992
A:Title: Structure, cloning, and expression of the gene for proteinase
A:Accession: A45080; M01D:93016043
A:Molecule type: DNA
A:Residues: 1-254, 'P' <STU>
A:Cross-references: CB:W97911
A:Note: sequence extracted from NCBI backbone (NCBIP:116205)
R:Zimmer, M.; Medcalf, R.L.; Pink, T.M.; Matmann, C.; Lichter, P.; Jenne, D.E.
Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992
A:Title: Three human A6268-like genes coordinately expressed in the myelomonocyte
A:Reference number: A6268; M01D:92390417
A:Accession: B46268

Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 1 NOGHEGALIHARFVMTASCRQ 25
20 nqgnicggallharvmtaascq 44

RESULT 15

AAV21551
ID AAV21551 standard; Protein: 225 AA.

AC AAV21551;

DT 03-AUG-1999 (first entry)

DE Human heparin-binding protein (HBP) signal, pro and mature sequence.

EA Heparin-binding protein; HBP; apoptosis; islets of Langerhans; beta cell;

EB endothelial cell; nerve cell; adipocyte; neurodegenerative disorder; cancer;

EC polyporphonuclear leukocyte; monocyte; neurodegenerative disorder; human;

ED proteoglycan; mitochondrial matrix targeting protein; viral infection;

EE apoptosis inhibitor; immune-mediated glomerulonephritis.

EF Homo sapiens.

EG W0992647-A1.

EH 03-JUN-1999.

FI 20-NOV-1998; 98MO-DK00510.

FJ 03-DEC-1997; 97DK-0001394.

FK 20-NOV-1997; 97DK-0001324.

FL (NCVO) NOVO-NORDISK AS.

FM Plodgaard HJ;

FN WPI: 1999-347615/29.

FO N-PSDB; AAK60695.

FP Modulating or decreasing apoptosis in cells useful for treating

PT neurodegenerative disorders and neuromuscular disorders

XX Claim 4, 5; Page 12; 74pp; English.

XX The invention relates to a new method of modulating or decreasing

XX apoptosis in mammalian beta cells of islets of Langerhans, endothelial

XX cells, and nerve cells. The method comprises administering a mammalian

XX heparin-binding protein (HBP) which is produced in the azurophilic granules

XX of polymorphonuclear leukocytes; and (iii) is a chemotactic agent for

XX monocytes. The new protein is useful for preventing or treating a

XX disorder (preferably in human patients) resulting from apoptosis of

XX mammalian cells, including insufficient functioning of insulin production

XX or insulin action, a neurodegenerative disorder, a neuromuscular

XX disorder, human immunodeficiency virus and ischemic stroke. Compositions

XX comprising the HBP and a proteoglycan which binds the HBP; and (b)

XX comprising the HBP and a proteoglycan which binds the HBP; and (b)

XX modulating or decreasing apoptosis in mammalian beta cells of islets of

XX Langerhans, endothelial cells or nerve cells. Unlike prior inhibitors,

XX the new apoptosis inhibitor does not cause disorders associated with the

XX inhibition of apoptosis such as cancer, autoimmune disorders such as

XX systemic lupus erythematosus, immune-mediated glomerulonephritis, and

XX viral infections. The present sequence represents the human HBP

XX signal sequence, prosequence and the mature sequence.

XX Sequence 225 AA;

Query Match 100.0%; Score 138; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 1 NOGHEGALIHARFVMTASCRQ 25
20 nqgnicggallharvmtaascq 44

Search completed: April 5, 2002, 14:59:47
Job time: 661 sec

PX	
PR	17-MAR-1988; 88DK-0001453.
XX	
XX	(NORD-) NORDISK GEOTERF E A/S.
XX	
PI	Fjordgaard H., Ostergaard E., Thomsen J., Bayne S;
XX	
DR	WPI; 1989-292496/40.
XX	
PT	Heparin-binding protein - having specified mol. wt. and exhibiting
PX	antigenic properties <i>in vivo</i> .
XX	
XX	Claim 10; page 47; 58pp; English.
XX	
XX	The sequence is that of human heparin binding protein (HBP). Amino
CC	acids X94, X98, and X11 are identical to those of the protein from Homo
CC	sapiens X74 and X75 are unknown. The no. amino acid position, 86-106,
CC	122, and 187 is unspecified. The HBP can be used to stimulate healing
CC	of chronic wounds, severe burns, or in tumour therapy.
XX	See also AAP08086.
XX	
Sequence	197 AA:

```

Query Match      100.00;  Score 138;  DB 10;
Best Local Similarity 100.00;  pval. No. 1.9e-09;
Matches 25;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1  NCGHRCGALIHARFPTASCTQ 25
        |||||||
Db       20  ngrhtllegaltharftymcaascfq 44

```

RESULT 11

AA084663 standard; protein; 221 AA.

AC AAR84663;
XX

DT 02-JUN-1996 (first entry)
YY

DE Human heparin-binding protein
yy

KW Heparin-binding protein; Gram-negative sepsis; septic shock; disseminated intravascular coagulation; endotoxaemia

Lipopolysaccharide-induced cytokine cascade disease: prevention; therapy.

XX	Homo sapiens
OS	

XX	Key	Location/Qualifiers
EH		

FT	
F1	20.:53
Replide	/notes "active fragment"

FT	peptide	26.:42	"/note-"	"active fragment"
FT				

```

ET      MISC-difference 100
ET      /label= Asn or Asp

```

11 /NOTE- ASU IN AAR84005 AND AAR84006
FT Misc-difference 104

```

/label=ash_of.asp
/note="Ser in AAR84665 and AAR84666"

```

```

      114 /label= Asn_or_Asp
      115
      116
      117
      118
      119
      120
      121
      122
      123
      124
      125
      126
      127
      128
      129
      130
      131
      132
      133
      134
      135
      136
      137
      138
      139
      140
      141
      142
      143
      144
      145
      146
      147
      148
      149
      150
      151
      152
      153
      154
      155
      156
      157
      158
      159
      160
      161
      162
      163
      164
      165
      166
      167
      168
      169
      170
      171
      172
      173
      174
      175
      176
      177
      178
      179
      180
      181
      182
      183
      184
      185
      186
      187
      188
      189
      190
      191
      192
      193
      194
      195
      196
      197
      198
      199
      200
      201
      202
      203
      204
      205
      206
      207
      208
      209
      210
      211
      212
      213
      214
      215
      216
      217
      218
      219
      220
      221
      222
      223
      224
      225
      226
      227
      228
      229
      230
      231
      232
      233
      234
      235
      236
      237
      238
      239
      240
      241
      242
      243
      244
      245
      246
      247
      248
      249
      250
      251
      252
      253
      254
      255
      256
      257
      258
      259
      260
      261
      262
      263
      264
      265
      266
      267
      268
      269
      270
      271
      272
      273
      274
      275
      276
      277
      278
      279
      280
      281
      282
      283
      284
      285
      286
      287
      288
      289
      290
      291
      292
      293
      294
      295
      296
      297
      298
      299
      300
      301
      302
      303
      304
      305
      306
      307
      308
      309
      310
      311
      312
      313
      314
      315
      316
      317
      318
      319
      320
      321
      322
      323
      324
      325
      326
      327
      328
      329
      330
      331
      332
      333
      334
      335
      336
      337
      338
      339
      340
      341
      342
      343
      344
      345
      346
      347
      348
      349
      350
      351
      352
      353
      354
      355
      356
      357
      358
      359
      360
      361
      362
      363
      364
      365
      366
      367
      368
      369
      370
      371
      372
      373
      374
      375
      376
      377
      378
      379
      380
      381
      382
      383
      384
      385
      386
      387
      388
      389
      390
      391
      392
      393
      394
      395
      396
      397
      398
      399
      400
      401
      402
      403
      404
      405
      406
      407
      408
      409
      410
      411
      412
      413
      414
      415
      416
      417
      418
      419
      420
      421
      422
      423
      424
      425
      426
      427
      428
      429
      430
      431
      432
      433
      434
      435
      436
      437
      438
      439
      440
      441
      442
      443
      444
      445
      446
      447
      448
      449
      450
      451
      452
      453
      454
      455
      456
      457
      458
      459
      460
      461
      462
      463
      464
      465
      466
      467
      468
      469
      470
      471
      472
      473
      474
      475
      476
      477
      478
      479
      480
      481
      482
      483
      484
      485
      486
      487
      488
      489
      490
      491
      492
      493
      494
      495
      496
      497
      498
      499
      500
      501
      502
      503
      504
      505
      506
      507
      508
      509
      510
      511
      512
      513
      514
      515
      516
      517
      518
      519
      520
      521
      522
      523
      524
      525
      526
      527
      528
      529
      530
      531
      532
      533
      534
      535
      536
      537
      538
      539
      540
      541
      542
      543
      544
      545
      546
      547
      548
      549
      550
      551
      552
      553
      554
      555
      556
      557
      558
      559
      560
      561
      562
      563
      564
      565
      566
      567
      568
      569
      570
      571
      572
      573
      574
      575
      576
      577
      578
      579
      580
      581
      582
      583
      584
      585
      586
      587
      588
      589
      590
      591
      592
      593
      594
      595
      596
      597
      598
      599
      600
      601
      602
      603
      604
      605
      606
      607
      608
      609
      610
      611
      612
      613
      614
      615
      616
      617
      618
      619
      620
      621
      622
      623
      624
      625
      626
      627
      628
      629
      630
      631
      632
      633
      634
      635
      636
      637
      638
      639
      640
      641
      642
      643
      644
      645
      646
      647
      648
      649
      650
      651
      652
      653
      654
      655
      656
      657
      658
      659
      660
      661
      662
      663
      664
      665
      666
      667
      668
      669
      670
      671
      672
      673
      674
      675
      676
      677
      678
      679
      680
      681
      682
      683
      684
      685
      686
      687
      688
      689
      690
      691
      692
      693
      694
      695
      696
      697
      698
      699
      700
      701
      702
      703
      704
      705
      706
      707
      708
      709
      710
      711
      712
      713
      714
      715
      716
      717
      718
      719
      720
      721
      722
      723
      724
      725
      726
      727
      728
      729
      730
      731
      732
      733
      734
      735
      736
      737
      738
      739
      740
      741
      742
      743
      744
      745
      746
      747
      748
      749
      750
      751
      752
      753
      754
      755
      756
      757
      758
      759
      760
      761
      762
      763
      764
      765
      766
      767
      768
      769
      770
      771
      772
      773
      774
      775
      776
      777
      778
      779
      780
      781
      782
      783
      784
      785
      786
      787
      788
      789
      790
      791
      792
      793
      794
```

FT	Misc-difference	145
7	20	20

/NOTE= "ASN IN 'AAR84665 AND AAR84666'"

PN W09528949-A1.

PD 02-NOV-1995.
xy

PF 17-MAR-1995; 95WO-DK00121.

XX	21-DEC-1994:	940K-0001452.
PR	21-APR-1994:	940K-0000464.
XX	(NOVO)	NOVO-NORDISK AS.
P1	Plodgaard HJH,	Rasmussen PB;
DR	WPI: 1995-382842/49.	
XX		
P7	Heparin-binding protein (HBP) composition - for prevention and	
PT	treatment of sepsis and other conditions.	
XX		
P5	Claim 3: Page 27-28: 48pp: English.	
XX		
CC	Heparin-binding protein (HBP) is produced by recombinant methods,	
CC	where host cells containing DNA encoding the HBP are cultured in an N-	
CC	terminal extension (see AM05128/705129 are cultured in a suitable	
CC	medium under conditions permitting HBP expression. The medium	
CC	contains a sulphated polysaccharide (heparin). Immobilised on an	
CC	inert carrier (agrose). To facilitate production of mature HBP, a	
CC	preferred DNA encodes an N-terminally extended HBP including a	
CC	protease cleavage site located between the N-terminal extension and	
CC	the mature HBP coding sequence, i.e. (Asp14)lys (enterokinase) or	
CC	ile-glu-gly-arg (factor-xa). HBP, or its fragments, is used in a	
CC	pharmaceutical composition for the prevention or treatment of	
CC	diseases associated with the sepsis syndrome, i.e. the negative sepsis,	
CC	septic shock, disseminated intravascular coagulation or	
CC	meningococcal meningitis.	
XX		
5Q	Sequence 221 AA:	
XX		
DB	Query Match: 100.0%; Score 138; DB 16; Length 221;	
XX	Best Local Similarity 100.0%; Pred. No. 4; 3e-09;	
XX	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 NCGRRPGCALHARWTFATASCG 25	
DB	20 ngrhtfcgallharwtfatascg 44	
XX		
RESULT 12		
ID	AA04875	
XX	AA04875 standard: protein; 221 AA.	
XX	AA04875:	
XX	20-DEC-1996 (first entry)	
DE	Heparin binding protein.	
KM	Heparin binding protein; conjugate; lipid; ceramide; analogue;	
KM	treatment; inflammation; viral infection; sepsis; septic shock;	
KM	ischemic reperfusion syndrome; immune system; stimulation;	
KM	protein phosphatase; disseminated intravascular coagulation.	
OS	Homo sapiens.	
PN	MO628544-AI.	
PO	19-SEP-1996.	
PE	11-MAR-1996; 96MO-DK00099.	
XX	09-MAR-1995; 95OK-0000240.	
PA	(NOVO) NOVO-NORDISK AS.	
XX	Plodgaard H, Rasmussen PB;	
PI	WPI: 1995-433819/43.	
OR		

RESULT 12

AAW04875 standard; protein; 221 AA

AC AA004875

DT 20-DEC-1996 (first entry)
xx

DE

YY

Heparin binding protein.

KM Heparin binding protein; conjugate; lipid; ceramide; analogue;
treatment; inflammation; viral infection; needle; needle stick

KM ischemic reperfusion syndrome; immune system; stimulation; myocardial infarction; disseminated intravascular coagulation

XX
XX
Homo sapiens

XX
XX
PN
W09628544-A1

XX
PD 19-SEP-1996.

AA 11-MAR-1996; 96MO-DK00099
PF

PR 09-MAR-1995; 95DK-0000240

PA (NOVO) NOVO-NORDISK AS.

PI Flodgaard H, Rasmussen PB;

DR WPT; 1996-433819/43.

DE	XX	CAP37 peptide analogue.
KM	XX	Cationic antimicrobial protein; CAP37, infection; septic shock;
KM	XX	treatment; prevention; prophylaxis; lipopolysaccharide endotoxin;
KM	XX	pathogen; analogue; human.
OS	XX	
OS	XX	Homo sapiens.
PN	XX	US6107460-A.
PD	XX	
PD	XX	22-AUG-2000.
PF	XX	01-MAR-1999; 99US-0258934.
PF	XX	01-MAR-1999; 99US-0258934.
PF	XX	(UYOK-) UNIV OKLAHOMA.
PI	XX	
PI	XX	Pereira HA.
DR	XX	MP1: 2000-578551/54.
DR	XX	
PT	XX	Novel peptide analogs derived from CAP37 peptides 23-42, comprising
PT	XX	serine or threonine substituted at one of two cysteine residues at
PT	XX	positions 26 and 42 useful for treating bacterial infections
PS	XX	
PS	XX	Disclousure: Columns 13-14; 40pp; English.
CC	XX	
CC	XX	Peptide derivatives based on the Cationic Antimicrobial Protein
CC	XX	(CAP37) peptide fragment comprising amino acids 23-42 are useful
CC	XX	for treating bacterial infections or treating or preventing septic
CC	XX	shock in a patient. Two new analogues of a larger peptide fragment
CC	XX	of CAP37, 20-44Ser26 and 20-44Ser26 were also active against
CC	XX	the gram-positive bacterial pathogens, Staphylococcus aureus and
CC	XX	Enterococcus faecalis and can bind and neutralise the toxic effects
CC	XX	of the LPS endotoxin. The peptides 20-44Ser26 and 20-44Ser42 can
CC	XX	be used to treat or prevent sepsis in a patient based on the synergic
CC	XX	The 20-44Ser26 and 20-44Ser42 peptides are based on the synergic
CC	XX	purity because the internal disulphide bond in between the two
CC	XX	cysteine residues can no longer occur. The solubility of these
CC	XX	two new peptides is also greater than the 20-44 peptide, enabling
CC	XX	their use at much higher concentrations than the 20-44 peptides.
CC	XX	See GENESEQ records AMB02021-BJ2078.
CC	XX	
CC	XX	Sequence 25 AA:
SO	XX	
SO	XX	Query Match
SO	XX	Best Local Similarity 100.0%: Score 138; DR 21; Length 25;
SO	XX	Matched 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SO	XX	
SO	XX	1 NQGRHFCGALHIAFQYMTASQFQ 25
SO	XX	1 nqgrhfcgallhafiymtaasqf 25
SO	XX	
SO	XX	Result 7
SO	XX	AMB09887
SO	XX	AMB09887 standard; peptide: 25 AA.
SO	XX	AMB09887:
SO	XX	
SO	XX	06-NOV-2000 (first entry)
SO	XX	
SO	XX	Cationic antimicrobial protein CAP37 peptide 20-44.
SO	XX	Cationic antimicrobial protein; CAP37, antibiotic; bacterial infection;
SO	XX	septic shock; wound healing; cancer.
SO	XX	Homo sapiens.
SO	XX	US6071879-A.

PD	06-JUN-2000.
PF	01-MAR-1999:
XX	99US-0260373.
XX	19-MAR-1992:
XX	92US-0855417.
PR	07-JUN-1995:
XX	95US-0482328.
PR	21-APR-1987:
XX	85US-0840919.
PR	25-JUL-1990:
XX	90US-0541353.
PR	30-OCT-1992:
XX	92US-0969931.
PR	29-APR-1994:
XX	94US-0235399.
PA	(OKLA) UNIV OKLAHOMA STATE.
P1	Perletra HA:
XX	WPI: 2000-450766/39.
XX	Treating endotoxic shock and infections caused by gram negative bacteria (e.g., Klebsiella, Pseudomonas, Escherichia coli or Salmonella)
P7	comprises administering antibiotic peptides derived from cationic Antilecithol protein 37 -
PS	Claim 1: Column 13-14: 23pp: English.
XX	The present sequence comprises amino acid residues 20-44 of the 37KD cationic antilecithol protein (CAP37). This protein has an antibacterial activity against both Gram positive and Gram negative bacteria as well as major reason for bacterial pathogenesis as the toxin can cause septic shock, the symptoms of which vary from chills and fever to circulatory failure and organ failure to death. This peptide can, therefore, be used CC to treat septic shock, to prevent its occurrence, and also to treat CC tumours and promote wound healing. The sequence is particularly useful CC for treating infection by gram negative bacteria such as Klebsiella, pseudomonas, E. coli, Bacteroides and Salmonella.
SQ	Sequence 25 AA:
DY	Query Match 100.0% Score 138: DB 21: Length 25: Best Local Similarity 100.0%: Pred. No. 7, 2e-10: Matches 25: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB	1 NCRRPFCGALTIHAFVFTASCFD 25 1 ngqrlhtgqalllharftvmtaaclq 25
RESULT 8	
AAB17394	
ID AAB17394 standard: Peptide: 25 AA.	
AC AAB17394:	
D7 31-OCT-2000 (first entry)	
DE CAP37 mimetic/LPS binding peptide sequence SEQ ID NO:498.	
KM Modified peptide: therapeutic agent; fusion; FC domain; cancer;	
KM autoimmune disease; cytotoxic; antitumour; thrombolytic; VEGF;	
KM immunosuppressive; EPO; TPO; CD44; mimetic; IL-1; TNF; antagonists;	
KM MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;	
KM cyclooxic T cell lymphocyte antigen 4; tumour necrosis factor;	
KM vascular endothelial growth factor; matrix metalloproteinase;	
KM asthma; thrombosis; pharmaceutical.	
OS Synthetic.	
PM WO2000024782-A2.	
XD 04-MAY-2000.	
XP 25-OCT-1999: 99NO-US25044.	

XX The peptide fragment of CAP37 has chemotactic activity for monocytes.
 CC It is especially useful for treating wounds or for dental
 CC applications. Other uses of CAP37 or its peptides include the
 CC treatment of cancer and any disease involving monocyte localization
 CC including deep-sea abscesses, osteomyelitis, endocarditis, rheumatoid
 CC arthritis and the treatment of endotoxemia. Specific CAP37
 CC peptides may be useful for treating infection due to antibacterial
 CC activity or for wound treatment because they possess antibacterial or
 CC lipopolysaccharide-binding activity. This sequence corresponds to
 CC residues 20-44 of mature CAP37. (See also AA01937-41934).
 XX

SQ Sequence 25 AA:

Query Match 100.0%: Score 138; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.2e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NQGRHFCGALIHARPYMTASCFQ 25
 |||
 Db 1 nqgrhfcgallharfymtasacfq 25

RESULT 2

AA026803: standard; peptide: 25 AA.

AA026803:

DT 03-NOV-1997 (first entry)

XX Human Cationic Antimicrobial Protein CAP37 amino acids 20-44.

XX Bacteriocide; septic shock; sepsis; bacterial lipopolysaccharide;
 KW LPS; binding; systemic vascular resistance; cardiac output;
 KW tissue perfusion; white blood cell count.

XX Homo sapiens.

XX US5650392-A.

XX 22-JUL-1997.

XX 05-JUL-1989; 89US-0375739.

XX 29-APR-1994; 94US-0235339.

XX 05-JUL-1989; 89US-0375739.

XX 25-JUN-1990; 90US-0543151.

XX 19-MAR-1992; 92US-0855417.

XX 30-OCT-1992; 92US-0859931.

XX 31-MAY-1995; 95US-0455485.

XX (OKLA) UNIV OKLAHOMA STATE.

XX Brackett DJ, Lerner MR, Pereira HA;

XX WPI: 1997-384696/35.

XX Peptide(s) derived from Cationic Antimicrobial Protein CAP37 -
 CC useful for treating septic shock and for treating
 CC physiological effects induced by a bacterial lipopolysaccharide in
 CC a mammal.

PS Claim 1: Columns 9-10; 18pp: English.

XX The present sequence corresponds to amino acid residues 20-44 from
 CC a naturally occurring Cationic Antimicrobial Protein of molecular
 CC weight 37 kd. The protein, designated CAP37, can be isolated from
 CC human neutrophils. The CAP37 (20-44) peptide is useful for treating
 CC or preventing septic shock. It can also be used for treating
 CC physiological effects induced by bacterial lipopolysaccharide in a
 CC mammal, e.g. on systemic vascular resistance, cardiac output, tissue

CC perfusion, and white blood cell count. The peptide has enhanced
 CC bacteriocidal activity compared to the native CAP37 and is active
 CC against gram-negative and gram-positive bacteria.

SQ Sequence 25 AA:

Query Match 100.0%: Score 138; DB 18; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.2e-10;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NQGRHFCGALIHARPYMTASCFQ 25
 |||
 Db 1 nqgrhfcgallharfymtasacfq 25

RESULT 3

AA015418: standard; peptide: 25 AA.

AA015418:

DT 05-JUN-1997 (first entry)

XX CAP37 fragment, 20-44.

XX Cationic antimicrobial protein; CAP37; bacterial lipopolysaccharide;
 KW LPS; septic shock; systemic vascular resistance; cardiac output;
 KW tissue perfusion; LPS-induced endotoxic response; antimicrobial;
 KW white blood cell count.

XX Synthetic.

XX US5607916-A.

XX 04-MAR-1997.

XX 05-JUL-1989; 89US-0375739.

XX 29-APR-1994; 94US-0235339.

XX 05-JUL-1989; 89US-0375739.

XX 25-JUN-1990; 90US-0543151.

XX 19-MAR-1992; 92US-0855417.

XX 30-OCT-1992; 92US-0859931.

XX (OKLA) UNIV OKLAHOMA STATE.

XX Brackett DJ, Lerner MR, Pereira HA;

XX WPI: 1997-164534/15.

XX Treating and preventing septic shock - by admin. of LPS-binding
 CC CAP37 protein fragment

PS Claim 2: Column 9-10; 19pp: English.

XX The sequences given in AA015418-19 represent fragments derived from
 CC cationic antimicrobial protein (CAP37). These peptides may be used for
 CC bacterial lipopolysaccharide (LPS). These peptides may be used for
 CC treating preventing or minimizing septic shock, treating physiological
 CC effects caused by bacterial LPS, treating the effects of LPS on systemic
 CC vascular resistance, cardiac output, tissue perfusion and white blood
 CC cell count. These peptides may be used for treating physiological effects
 CC induced by LPS in a test animal. These peptides show a strong
 CC antimicrobial activity. The peptides have enhanced bacteriocidal activity
 CC compared to full length CAP37 and are active against gram positive and
 CC gram negative bacteria. AA015418 is antimicrobial at concentrations of
 CC 1.25-7.5 x 10⁻⁵ and has maximum activity between pH 5 and pH 5.5.

Query Match 100.0%: Score 138; DB 18; Length 25;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

on protein - protein search, using SW model

Run on: April 5, 2002, 14:48:46 ; Search time 23.96 Seconds
(without alignments)
77.388 Million cell updates/sec

Title:	US-09-657-276-1032
Perfect score:	138
Sequence:	1 NQGRHFCGALIHARFVMTASCFQ 25

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing:	Minimum Match 0%
	Maximum Match 100%

Database

1.	<i>S1D58/gcgcda/genseq/gensep/AA1980.DAT</i>
2.	<i>S1D58/gcgcda/genseq/gensep/AA1991.DAT</i>
3.	<i>S1D58/gcgcda/genseq/gensep/AA1992.DAT</i>
4.	<i>S1D58/gcgcda/genseq/gensep/AA1993.DAT</i>
5.	<i>S1D58/gcgcda/genseq/gensep/AA1994.DAT</i>
6.	<i>S1D58/gcgcda/genseq/gensep/AA1995.DAT</i>
7.	<i>S1D58/gcgcda/genseq/gensep/AA1996.DAT</i>
8.	<i>S1D58/gcgcda/genseq/gensep/AA1997.DAT</i>
9.	<i>S1D58/gcgcda/genseq/gensep/AA1998.DAT</i>
10.	<i>S1D58/gcgcda/genseq/gensep/AA1999.DAT</i>
11.	<i>S1D58/gcgcda/genseq/gensep/AA1990.DAT</i>
12.	<i>S1D58/gcgcda/genseq/gensep/AA1991.DAT</i>
13.	<i>S1D58/gcgcda/genseq/gensep/AA1992.DAT</i>
14.	<i>S1D58/gcgcda/genseq/gensep/AA1993.DAT</i>
15.	<i>S1D58/gcgcda/genseq/gensep/AA1994.DAT</i>
16.	<i>S1D58/gcgcda/genseq/gensep/AA1995.DAT</i>
17.	<i>S1D58/gcgcda/genseq/gensep/AA1996.DAT</i>
18.	<i>S1D58/gcgcda/genseq/gensep/AA1997.DAT</i>
19.	<i>S1D58/gcgcda/genseq/gensep/AA1998.DAT</i>
20.	<i>S1D58/gcgcda/genseq/gensep/AA1999.DAT</i>
21.	<i>S1D58/gcgcda/genseq/gensep/AA2000.DAT</i>
22.	<i>S1D58/gcgcda/genseq/gensep/AA2001.DAT</i>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	138	100.0	25	14	AA941934	Peptide fragment c
2	138	100.0	25	18	AAW26803	Human Cationic
3	138	100.0	25	18	AAW15418	CP37 fragment, 20
4	138	100.0	25	21	AAW97174	Peptide derived for
5	138	100.0	25	21	AA828489	Human 14popolysacc
6	138	100.0	25	21	AA802021	CP37 peptide analo
7	138	100.0	25	21	AA809887	Cationic antimicro
8	138	100.0	25	21	AA817394	CP37 mimetic/APS
9	138	100.0	25	22	AA891856	Antimicrobial pep
10	138	100.0	197	10	AA891381	Human heparin bin
11	138	100.0	221	16	AA841663	Human heparin bin

12	138	100.0	2.21	17	AAH04875	Hepatitis binding protein
13	138	100.0	2.22	20	AAH14935	Recombinant catenin
14	138	100.0	2.22	20	AAH72210	CAP37 protein, Homo
15	138	100.0	2.22	20	AAH721551	Hepatitis-B-binding
16	138	100.0	2.25	20	AAH881318	Mature human heparin
17	138	100.0	2.25	20	AAH883362	Mature human heparin
18	138	100.0	2.25	21	AAH718878	Mature human heparin
19	138	100.0	2.25	21	AAH718883	Mature human heparin
20	138	100.0	2.25	21	AAH717884	Mature human heparin
21	138	100.0	2.25	12	AAH778891	Mature human heparin
22	138	100.0	2.26	12	AAH106659	Catonic granule p
23	138	100.0	2.32	20	AAH215550	Mature human heparin
24	138	100.0	2.32	20	AAH881250	Mature human heparin
25	138	100.0	2.32	20	AAH883364	Mature human heparin
26	138	100.0	2.44	22	AAH718877	Mature human heparin
27	138	100.0	2.44	22	AAH718893	Mature human heparin
28	138	100.0	2.51	12	AAH106688	Catonic granule p
29	138	100.0	2.51	16	AAH886656	Mature human heparin
30	138	100.0	2.51	16	AAH881252	Mature human heparin
31	138	100.0	2.51	21	AAH883365	Mature human heparin
32	138	100.0	2.51	21	AAH718884	Mature human heparin
33	138	100.0	2.51	21	AAH718894	Mature human heparin
34	138	100.0	2.74	16	AAH886658	Mature human heparin
35	137	99.3	2.5	21	AAH802055	Mature human heparin
36	135	97.8	2.5	21	AAH802056	Mature human heparin
37	135	97.8	2.5	21	AAH802057	Mature human heparin
38	135	97.8	2.5	21	AAH802060	Mature human heparin
39	135	97.8	2.5	21	AAH802061	Mature human heparin
40	135	97.8	2.5	21	AAH802062	Mature human heparin
41	134	97.1	2.5	21	AAH802071	Mature human heparin
42	134	97.1	2.5	21	AAH802075	Mature human heparin
43	133	96.4	2.5	21	AAH802059	Mature human heparin
44	133	96.4	2.5	21	AAH802030	Mature human heparin
45	132	95.7	2.5	21	AAH802047	Mature human heparin

ALIGNMENTS

[illegible]

AC MAR41934;

DE Peptide fragment of mature CAP37 protein

KW endotoxaemia.

OS Homo sapiens

PN W09319087-A.

PD 30-SEP-1993

PF 19-MAR-1993

PR	19-MAR-1992;	9205-0855417
YY		

PA (01EM-) UNIV EMORY SCHOOL MI
XX

PI PERELA HA, SPILZNGEL ON;
XX

[illegible]

PT and Lipo:polysaccharide

PS Claim 9; page 72; 109pp; English.

Best Local Similarity 100.0%; Pred. No. 7.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NCGRRFCGALIHARFVMTAASCFQ 25
DB 1 ngrhfcgallharfvmataascf 25

RESULT 4

AAW97174 standard; peptide: 25 AA.
XX
AC AAW97174;
XX
DT 30-APR-1999 (first entry)
XX
DE Peptide derived from residues 20-44 of mature CAP37.
XX
XX CAP37; Cationic antimicrobial protein antibiotic; human;
XX antimicrobial; endotoxin; tumor necrosis factor alpha;
XX TNF-alpha; endotoxic shock; septic shock; gram negative bacteria.
XX
OS Homo sapiens.
XX
PM US5877151-A.
XX
PD 02-MAR-1999.
XX
PP 21-APR-1997; 9705-0840519.
XX
PR 07-JUN-1985; 95US-0482328.
XX 05-JUL-1985; 89US-0175739.
XX 25-JUN-1990; 90US-0543151.
XX 19-MAR-1992; 92US-0855417.
XX 30-OCT-1992; 92US-0965931.
XX 29-APR-1994; 94US-0235399.
XX 21-APR-1997; 97US-0840519.
XX
PA (OKLA) UNIV OKLAHOMA STATE.
XX
XX
XX Pereira HA;
XX
XX WPI: 1999-189693/16.
XX
XX Inhibiting tumor necrosis factor alpha production - using peptides
XX derived from cationic antimicrobial protein CAP37, e.g. to treat
XX sepsis
XX
XX Claim 1; Column 5; 29pp; English.
XX
XX The present sequence represents a peptide derived from residues 20-44 of
XX a protein called CAP37 (cationic antimicrobial protein, having a
XX molecular weight of about 37 kDa) which is a secreted protein and is a
XX chemottractant for monocytes and can bind to lipopolysaccharide and
XX human neutrophils. The present peptide also has strong antimicrobial
XX activity, and can be used to reduce endotoxin-induced production of
XX tumour necrosis factor (TNF)-alpha. The peptide is useful for treating
XX ongoing endotoxic (septic) shock and to prophylactically treat an
XX individual who may have a risk of septic shock prior to a surgical
XX procedure such as bowel or bladder surgery or surgical manipulation
XX of other organs where gram negative bacteria normally reside and could
XX enter the bloodstream.
XX
XX Sequence 25 AA:

Query Match 100.0%; Score 138; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NCGRRFCGALIHARFVMTAASCFQ 25
DB 1 ngrhfcgallharfvmataascf 25

DB 1 ngrhfcgallharfvmataascf 25

RESULT 5
AAW97174 standard; peptide: 25 AA.
XX
AC AAW97174;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human lipopolysaccharide binding protein #1.
XX
XX Human; lipopolysaccharide binding protein; lipopolysaccharide analogue;
XX LPSA; immunosay; gram-negative bacterium detection; Escherichia coli;
XX Salmonella; Chlamydia; Infection.
XX
XX Homo sapiens.
XX
XX W0200060354-A1.
XX
PD 12-OCT-2000.
XX
PP 03-APR-2000; 2000WO-EP02869.
XX
PP 07-APR-1999; 99EP-0302711.
XX
PA (UNITL) UNILEVER PLC.
XX (UNITL) UNILEVER NV.
XX (HIND-) HINDUSTAN LEVER LTD.
XX
PI Badley RA, Hughes G, Zak KM;
XX
XX WPI: 2000-679390/66.
XX

Immunosay for detecting lipopolysaccharides (LPS) from gram negative
bacteria in a sample, comprises use of LPS-binding protein and an
antibody to LPS as first or second binding reagents -

Claim 12; Page 13; 40pp; English.

The present sequence is lipopolysaccharide binding protein which may be
used for detecting the presence of a lipopolysaccharide analyte (LPSA) in
a sample. Anti-LPSA antibody is also used to detect the LPSA. The
immunosay is useful for detecting the presence of LPSA derived from the
cell membrane of a gram-negative bacterium such as Escherichia coli,
Salmonella and Chlamydia. It provides for assay devices to be
constructed which are capable of accurate and reproducible test
results, ideally suited for commercial markets such as the clinical or
home-testing markets. Furthermore, such immunosays can be performed
quickly and simply, without using complex extracts or multiple assay
steps.

Sequence 25 AA:

Query Match 100.0%; Score 138; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e-10;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NCGRRFCGALIHARFVMTAASCFQ 25
DB 1 ngrhfcgallharfvmataascf 25

RESULT 6

AAW02021 standard; peptide: 25 AA.
XX
AC AAW02021;
XX
XX 03-JAN-2001 (first entry)
XX

XX	23-OCT-1998:	980S-0105371.
PR	23-OCT-1999:	990S-0428082.
XX	(AMGE-) AMGEN INC.	
PA-	Pelige U,	Liu C, Cheetham J, Boone TC;
PI	WPI: 2000-350702/30.	
DR	Novel composition of matter comprising an FC domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -	
XX	Claim 39; Page 370; 608pp; English.	
XX	The present invention describes composition of matter (i) comprising an FC domain, pharmacologically active peptide sequences, and disease (ii) is: (X1)a-p1-(X2)b, where: p1 = an FC domain in X1 and X2 are each independently selected from: -(L1)c-p1, -(L1)c-p1-(L2)d-p2, -(L1)c-p1-(L2)d-p2-(L3)e-p3, or -(L1)c-p1-(L2)d-p2-(L3)e-p3-(L4)f-p4 where p1, p2, p3, and p4 = are each independently sequences of pharmacologically active peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can include anticancer, antitubercular, thrombolytic and immunosuppressive agents. The present invention can be used for treating pharmaceutical compositions, or autoimmune diseases useful for treating cancer, sepsis, thrombosis, or autoimmune diseases. The use of an FC domain (rather than a Fab domain) can provide a longer half-life or incorporate functions such as Fc receptor binding, protein A binding, complement fixation, and possibly placental transfer. AA69443 to AA69536 and AA69535 to AA69503 represent nucleotide and amino acid sequences used in the exemplification of the present invention.	
CC	Sequence	25 AA:
XX		
XX		
Query Match	100.0%	Score 138; DB 21; Length 25;
Beat Local Similarity	100.0%;	Pred. No. 7.2e-10;
Matches	25; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Dh	1 NCGRRPGGALIHARPPVFAASCPD 25 1 ngrfnlcggallharfivmctasacfd 25	
RESULT 9		
AA691856	AB691856 standard; Peptide: 25 AA.	
AC	AB691856;	
XX	23-JUN-2001 (first entry)	
DR	Antimicrobial peptide SEQ ID NO:10332.	
XX		
KM	Protection: endogenous therapeutic peptide; peptidase; conjugation; blood component; modification: succinimidyl; maleimido group; amino hydroxyl; thiol; hormone; growth factor; neurotransmitter.	
XX	Homo sapiens.	
OS	Synthetic.	
XX	MO200005900-A2.	
PA	23-NOV-2000.	
PD	17-MAY-2000; 2000MO-USI3576.	
PE	17-MAY-1999; 990S-0134406.	
PR	10-SEP-1999; 990S-0153406.	
PR	15-OCT-1999; 990S-0159783.	

XX	PA	(CONJ.) CONJUCHEM INC.
XX	PA	Bridon DP, Earin AM, Milner PC, Holmes DL, Thibodeau K:
XX	DR	WPI: 2001-112059/12.
XX	XX	
XX	XX	Modifying and attaching therapeutic peptides to albumin prevents
XX	XX	peptidase degradation, useful for increasing length of in vivo activity
XX	XX	
XX	PS	Disclosure: Page 533: 733pp: English.
XX	XX	
CC	CC	The present invention describes a modified therapeutic peptide (1)
CC	CC	comprising a therapeutically active amino acid region (iii) and a
CC	CC	reactive group (ii) (e.g. succinimidyl and maleimido groups) attached to
CC	CC	a less therapeutically active amino acid region (iv), which covalently
CC	CC	bonds to albumin/hydroxy/thiol groups on blood components to form a
CC	CC	peptide-albumin conjugate. The peptide (1) is useful for modifying the
CC	CC	factor and neurotensin, to protect them from peptidase activity
CC	CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	CC	peptides are not suitable as drug candidates as they require frequent
CC	CC	administration due to rapid degradation by peptidases in the body.
CC	CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	CC	reduces the action of peptidases to increase length of activity (half
CC	CC	life) and specifically as bonding to large molecules decreases
CC	CC	Abb90829 to Abb9243 represent peptides which can be used in the
CC	CC	exemplification of the present invention.
XX	XX	
XX	XX	Sequence 25 AA:
XX	XX	
XX	XX	Query Match 100.0%: Score 138; DB 22; Length 25;
XX	XX	Best Local Similarity 100.0%: Pred. No. 7, 2e-10;
XX	XX	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	OY	1 NCGRHRCGGALIAAPFWTAAASCO 25
OY	OY	
DB	DB	1 ngrhrcggaliharfwmtaacdq 25
XX	XX	
XX	XX	RESULT 10
XX	XX	AAp91931 standard: protein. 197 AA.
XX	XX	AAp91931:
XX	XX	06-FEB-1990. (first entry)
XX	XX	
XX	XX	Human heparin binding protein.
XX	XX	
XX	XX	Heparin binding protein: angiogenic.
XX	XX	
XX	XX	Homologous.
XX	XX	
XX	XX	Key Location/Qualifiers
XX	XX	Modified-site 94
XX	XX	Modified-site 98
XX	XX	Modified-site 131
XX	XX	Region 74-75
XX	XX	Region 153
XX	XX	Region 162
XX	XX	Region 167
XX	XX	Region 167
XX	XX	
XX	XX	MO8908666-A.
XX	XX	
XX	XX	21-SEP-1989.
XX	XX	
XX	XX	17-MAR-1989; B9WO-DK00059.
XX	XX	

XX Conjugate of heparin binding protein with ceramide analogue - used
 PT to treat conditions involving stress injury to cells e.g.
 PT inflammation, viral infection, sepsis and septic shock
 XX
 XX Disclosure: Page 22-23: 39pp: English.
 CC Heparin binding protein conjugated to a ceramide analogue may be
 CC used in the prevention or treatment of inflammation, viral infection,
 CC ischaemic reperfusion syndrome, sepsis, septic shock, disseminated
 CC intravascular coagulation or for stimulating a patient's immune
 CC system. When the conjugate is contacted with living cells, the
 CC lipid containing ceramide analogue activates a ceramide activated
 CC protein phosphatase which results in down-regulation of cellular
 CC metabolism.
 CC
 XX Sequence 221 AA:
 SO

Query Match 100.0%: Score 138: DB 17: Length 221:
 Best Local Similarity 100.0%: Pred. No. 4.3e-09:
 Matches 25: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 NCGRRFCGALIHARFVMTASCFQ 25
 DB 20 ngrhfcgallharfvmtascfq 44

RESULT 13
 AAM73210
 ID AAM73210 standard: peptide: 222 AA.
 AC AAM73210:
 XX
 XX AAM73210:
 DT 19-APR-1994 (first entry)
 XX
 XX Recombinant cationic granule protein (CAP37).
 XX
 XX Peptide: CAP37; cancer; monocytes; chemotaxis; wound healing;
 XX antibacterial; infection; neoplastic disease; parasitic disease;
 XX endotoxaemia; STD; herpes simplex.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO319087-A.
 XX
 XX 30-SEP-1993.
 XX
 XX 19-MAR-1993: 93MO-US02580.
 XX
 XX 19-MAR-1992: 92US-0855417.
 XX
 XX (UTEM-) UNIV EMORY SCHOOL MEDICINE.
 XX
 XX Pereira HM, Splitznagel JK;
 XX
 XX MPI: 1993-320680/40.
 XX
 XX
 XX Peptide fragments of CAP37 protein - with chemotactic, antibiotic
 XX and lipopolysaccharide-binding activities
 XX
 XX Disclosure: Page 73: 109pp: English.
 XX
 XX CAP37 has chemotactic activity for monocytes, is bactericidal and
 XX is capable of binding bacteria lipopolysaccharide.
 XX It is especially useful for treatment of wounds and for dental
 XX applications. Other uses of CAP37 or its peptides include the
 XX treatment of cancer and any disease involving monocyte localization
 XX including neoplastic diseases, parasitic diseases and rheumatoid
 XX arthritis. CAP37 may also be used to treat diseases involving
 XX defects of monocyte chemotaxis such as chronic mucocutaneous
 XX candidiasis, SLE and herpes simplex. Specific CAP37 peptides may
 XX be useful for treating infection due to antibacterial activity or

CC for wound treatment because they possess antibiotic or
 CC lipopolysaccharide-binding activity. CAP37 and constituent
 CC peptides may also be used to treat endotoxaemia. The recombinant
 CC CAP37 molecule can have N-terminal extensions added to it, these
 CC being either a single methionine residue or the sequence described
 CC in file AAM73210.
 XX
 XX Sequence 222 AA:
 SO

Query Match 100.0%: Score 138: DB 14: Length 222:
 Best Local Similarity 100.0%: Pred. No. 4.3e-09:
 Matches 25: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 NCGRRFCGALIHARFVMTASCFQ 25
 DB 20 ngrhfcgallharfvmtascfq 44

RESULT 14
 AAM73210
 ID AAM73210 standard: peptide: 222 AA.
 AC AAM73210:
 XX
 XX AAM73210:
 DT 22-JAN-1999 (first entry)
 XX
 XX CAP37 protein.
 XX
 XX Defensin: T-cell chemotaxis; therapy; immune response induction; tumour;
 XX antigenic agent; infection; hyperproliferative disorder; CAP37;
 XX immunodeficiency.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US5837247-A.
 XX
 XX 17-NOV-1998.
 XX
 XX 16-JUN-1995: 95US-0491204.
 XX
 XX 16-JUN-1995: 95US-0491204.
 XX
 XX (USSM) US PUBLIC HEALTH SERVICE NAT INST HEALTH.
 XX
 XX Chertov O, Michiel D, Murphy WJ, Oppenheim JJ, Taub DD;
 XX Wang JW, Xu L;
 XX
 XX MPI: 1999-023377/02.
 XX
 XX Use of defensin proteins - for inducing or stimulating T-cell
 XX chemotaxis used for treating infections, tumours, immunodeficiencies
 XX or autoimmune conditions
 XX
 XX Disclosure: Column 25-28: 20pp: English.
 XX
 XX This sequence represents the CAP37 protein, and can be used
 XX in the method of the invention. The method is for inducing or
 XX stimulating T-cell chemotaxis in a subject, comprising administering to
 XX the subject a pharmaceutical composition comprising a defensin protein.
 XX The method can be used for inducing an immune response in a subject to an
 XX antigenic agent such as tumour, infectious agent or other diseases
 XX tissue. The method can also be used to treat e.g. bacterial, viral,
 XX fungal and other infections, tumours and other hyperproliferative
 XX disorders, immunodeficiencies, diseases susceptible to treatment by
 XX administration of a therapeutic vaccine and autoimmune conditions. The
 XX peptides can also be used to treat inflammation or autoimmune
 XX conditions.
 XX
 XX Sequence 222 AA:
 SO

Query Match 100.0%: Score 138: DB 20: Length 222:

Gencode version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: April 5, 2002, 14:57:46 : Search time 12.8 seconds
(without alignments)

148,778 Million cell updates/sec

Title: US-09-657-276-1032

Sequence: 1 NCGRHFGCALIHARFVMAACSTQ 25

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR-68.1

1: p1r1:
2: p1r2:
3: p1r3:
4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	251	1 TRHUAZ	azurocidin precursor
2	103	74.6	219	1 TRPGAT	azurocidin - p19
3	93	67.4	256	1 PRHJ3	proteolase 3 (EC 3
4	85	61.6	231	1 TRPCTR	trypsin (EC 3.4.21
5	85	61.6	248	2 S55066	trypsin (EC 3.4.21
6	85	61.6	258	2 I56220	trypsin (EC 3.4.21
7	85	61.6	270	2 S56160	mast cell tryptase
8	84	60.9	229	1 TRBUTR	trypsin (EC 3.4.21
9	84	60.9	241	1 TRBCTR	trypsin (EC 3.4.21
10	84	60.9	247	2 S13813	trypsin (EC 3.4.21
11	84	60.9	247	2 S13813	trypsin (EC 3.4.21
12	83	60.1	247	2 A27547	trypsin (EC 3.4.21
13	83	60.1	248	2 S55067	trypsin (EC 3.4.21
14	83	60.1	711	1 A47136	macrophage-stimula
15	82	59.4	455	2 A61545	plasma (EC 3.4.21
16	81	58.7	246	1 TRRT2	trypsin (EC 3.4.21
17	81	58.7	246	1 TRRT2	trypsin (EC 3.4.21
18	81	58.7	247	2 S12764	trypsin (EC 3.4.21
19	81	58.7	259	2 S13863	trypsin (EC 3.4.21
20	81	58.7	259	2 S13863	trypsin (EC 3.4.21
21	80	58.0	242	2 S13775	macrophage-stimula
22	80	58.0	242	2 S13775	trypsin (EC 3.4.21
23	80	58.0	242	2 S49489	trypsin (EC 3.4.21
24	80	58.0	242	2 S13776	trypsin (EC 3.4.21
25	80	58.0	246	2 B25528	trypsin (EC 3.4.21
26	80	58.0	273	2 A47246	trypsin (EC 3.4.21
27	80	58.0	274	2 A45754	trypsin (EC 3.4.21
28	80	58.0	274	2 JC4171	trypsin (EC 3.4.21
29	80	58.0	275	2 A35863	trypsin (EC 3.4.21

30	80	58.0	275	2 B35863	trypsin (EC 3.4.21
31	80	58.0	275	2 C35863	trypsin (EC 3.4.21
32	80	58.0	276	2 A38654	mast cell protease
33	79.5	57.6	558	1 JC5878	plasma hyaluronan-
34	79.5	57.6	560	1 JC4795	hypothetical prote
35	79	57.2	186	2 T08808	trypsin-like prote
36	79	57.2	256	1 B35471	macrophage-stimula
37	79	57.2	275	2 A32410	trypsin (EC 3.4.21
38	79	57.2	275	2 A32410	trypsin (EC 3.4.21
39	79	57.2	1420	2 A32869	apolipoprotein(a)
40	78	56.5	229	1 TRDPS	trypsin (EC 3.4.21
41	78	56.5	237	2 S68702	trypsin (EC 3.4.21
42	78	56.5	243	2 A35871	trypsin (EC 3.4.21
43	78	56.5	247	1 A25852	trypsin (EC 3.4.21
44	78	56.5	247	1 TRDC	trypsin (EC 3.4.21
45	78	56.5	249	2 A55634	granzyme M (EC 3.4

ALIGNMENTS

RESULT 1

TRHUAZ

azurocidin precursor (validated) - human

N:Alternate names: cationic antimicrobial protein CAP37; heparin-binding protein; ne

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992; sequence-revision 30-Sep-1993; text-change 08-Dec-2000

C:Accession: A46268; A46455; S16450; S18820; S12881; S14445; S14738; B33913; A60708;

R:Zimmer, M.; Medcalf, R.L.; Fink, T.M.; Maltmann, C.; Lichter, P.; Jenne, D.E.

Proc. Natl. Acad. Sci. U.S.A. 89, 8215-8219, 1992

A>Title: Three human elastase-like genes coordinately expressed in the myelomonocyte

A:Reference number: A46268; M01D:92390417

A:Molecule type: cDNA

A:Residues: 1-251 <21N>

A:Cross-references: GR:M69326; M1D:9179301; P1D:N:A859333.1; P1D:9179302

A:Note: sequence extracted from NCBI backbone (NCBIN:112883; NCBIN:112891; NCBIN:112

R:Morgan, J.G.; Suklenick, T.; Pereira, H.A.; Spliznagel, J.K.; Guerra, M.E.; Latr

J. Immunol. 147, 3210-3214, 1991

A>Title: Cloning of the cDNA for the serine protease homolog CAP37/azurocidin, a mic

A:Reference number: A46455; M01D:92013155

A:Accession: A46455

A:Molecule type: mRNA

A:Residues: 3-251 <21N>

A:Cross-references: GR:M69326; M1D:9179301; P1D:N:A859333.1; P1D:9179302

A:Note: sequence extracted from NCBI backbone (NCBIN:60386; NCBI:P:60395)

R:Almeida, R.P.; Melchior, M.; Campanelli, D.; Nathan, C.; Gabey, J.E.

Biochem. Biophys. Res. Commun. 177, 688-695, 1991

A>Title: Complementary DNA sequence of human neutrophil azurocidin, an antidiabetic w

A:Reference number: S16450; M01D:91264832

A:Accession: S16450

A:Molecule type: mRNA

A:Residues: 3-251 <21N>

A:Cross-references: EMBL:X58794; M1D:928976; P1D:N:CMA1601.1; P1D:928977

A:Accession: S18520

A:Molecule type: protein

A:Residues: 47-51, 'S', '53-59, 'T', '61-62, 'V', '64-87 <ALZ>

R:Polh, J.; Pereira, H.A.; Martin, N.M.; Spliznagel, J.K.

FEBS Lett. 272, 200-204, 1990

A>Title: Amino acid sequence of CAP37, a human neutrophil granule-derived antibacter

A:Reference number: S12881; M01D:91032128

A:Accession: S12881

A:Molecule type: protein

A:Residues: 27-248 <21N>

R:Polh, J.; Pereira, H.A.; Martin, N.M.; Spliznagel, J.K.

FEBS Lett. 272, 200-204, 1990

A>Title: Covalent structure of two novel neutrophil leucocyte-derived proteins of f

A:Reference number: S15393; M01D:91224149

A:Accession: S15445

A:Molecule type: protein

A:Residues: 27-129, 'N', '131-247 <FLD>

A:Note: the sequence from Fig. 7 is inconsistent with that from Fig. 6 in having 19C

A: Molecule type: DNA
 A: Residues: 1-118, 'V', 120-134, 'AT', 137-256 <ZIM>
 A: Note: Sequence extracted from NCBI backbone (NCBIN:112898, NCBIN:112900, NCBIN:112902, Rikshaw, C.; Musette, P.; Cayre, Y.E. 1990).
 A: Title: Megener's autoantigen and leukemia.
 A: Reference number: A43983; MUID:92021008
 A: Accession number: A43983
 A: Molecule type: mRNA
 A: Residues: 1-69, 'P', 71-256 <LA2>
 A: Cross-references: GB:W5154; NID:9187398; PIDN:AAA59558.1; PID:9187399
 R: Campanelli, D.; Melchior, M.; Pu, Y.; Nakata, M.; Shuman, H.; Nathan, C.; Gabay, J.E.
 J. Exp. Med. 172, 1709-1715, 1990
 A: Title: Cloning of cDNA for proteinase 3, a serine protease, anti-biotic, and autoantigen
 A: Reference number: JH0331; MUID:91079774
 A: Accession number: JH0331
 A: Molecule type: mRNA
 A: Residues: R, 3-118, 'V', 120-134, 'AT', 137-256, 'P', <CAN>
 A: Cross-references: GB:W5154; NID:9187398; PIDN:AAA59558.1; PID:9187399
 A: Note: part of this sequence including the mature protein, was confirmed by the authors translated the codon GCG for residue 49 as GGU, GGC for residue 52 and
 R: Borles, D.; Baynal, M.C.; Solomon, D.H.; Datzynkiewicz, Z.; Cayre, Y.E.
 Cell 59, 959-968, 1989
 A: Title: Down-regulation of a serine protease, myeloblastin, causes growth arrest and death
 A: Reference number: A43751; MUID:9009622
 A: Accession number: A43751
 A: Molecule type: mRNA
 A: Residues: 42-235 <BOB>
 A: Cross-references: GB:W5154; NID:9187398; PIDN:AAA59558.1; PID:9187399
 A: Note: The authors translated the codon GCG for residue 49 as GGU, GGC for residue 52 and
 R: Borles, D.; Baynal, M.C.; Solomon, D.H.; Datzynkiewicz, Z.; Cayre, Y.E.
 Cell 59, 959-968, 1989
 A: Title: Megener's autoantigen decoded.
 A: Reference number: S11091; MUID:90332035
 A: Accession number: S11091
 A: Molecule type: mRNA
 A: Residues: 20-56 <JEN>
 R: Musette, P.; Labbaye, C.; Dorner, M.R.; Cayre, Y.E.; Casanova, J.L.; Kourilsky, P.
 Blood 77, 1398-1399, 1991
 A: Title: Megener's autoantigen and leukemia.
 A: Reference number: A61176; MUID:9113650
 A: Accession number: A61176
 A: Molecule type: mRNA
 A: Residues: 1-42 <MUS>
 A: Cross-references: EMBL:X56606; NID:935189; PIDN:CAA39943.1; PID:935190
 R: Goldschmidt, R.; Dolman, K.M.; Van Den Ende, M.E.; Van Der Meer-Ceritsen, C.H.; Sor
 APMS 19(Suppl.), 26-27, 1990
 A: Title: The relation of 29 kD C-ANCA antigen to proteinase 3.
 A: Reference number: A60148; MUID:91136884
 A: Accession number: A60148
 A: Molecule type: protein
 A: Residues: 28-61, 'X', 63, 'D', 65-67, 228-244 <RAO>
 R: Ballester, J.; Nebreda, J.G.; Marshall, B.C.; Gray, W.R.; Gray, B.H.; Hoidal, J.R.
 J. Biol. Chem. 266, 9540-9548, 1991
 A: Title: Characterization of proteinase-3 (PR-3), a neutrophil serine proteinase. Struct
 A: Reference number: A43982; MUID:91236723
 A: Accession number: A43982
 A: Molecule type: protein
 A: Residues: 28-61, 'X', 63, 'D', 65-67, 228-244 <RAO>
 R: Ballester, J.; Nebreda, J.G.; Marshall, B.C.; Gray, W.R.; Gray, B.H.; Hoidal, J.R.
 J. Biol. Chem. 266, 9540-9548, 1991
 A: Title: Characterization of two neutrophil granule proteases with active-site homology to
 A: Reference number: A43981; MUID:90130450
 A: Accession number: A43981
 A: Molecule type: protein
 A: Residues: 28-45, 'P', 47, 196-208, 'X', 210-215, 'X', 217-219 <MT>
 R: Gabay, J.E.; Scott, R.W.; Campanelli, D.; Griffith, J.; Wilde, C.; Morra, M.N.; Seeger
 Proc. Natl. Acad. Sci. U.S.A. 86, 5610-5614, 1989
 A: Title: Antibiotic proteins of human polymorphonuclear leukocytes.
 A: Reference number: A43913; MUID:89315847
 A: Accession number: C33913
 A: Molecule type: protein
 A: Residues: 28-45, 'E', 47 <GAB>
 R: Riles, J.L.; McCluskey, R.T.; Ahmad, M.F.; Arnaut, M.A.

Blood 74, 1888-1893, 1989
 A: Title: Megener's autoantigen is a novel neutrophil serine proteinase
 A: Reference number: A60481; MUID:90028708
 A: Accession number: A60481
 A: Molecule type: protein
 A: Residues: 28-30, 'X', 40-47 <MT>
 R: Ballester, J.; Nebreda, J.G.; Marshall, B.C.; Gray, W.R.; Gray, B.H.; Hoidal, J.R.
 J. Biol. Chem. 266, 9540-9548, 1991
 A: Title: Monoclonal antibodies specific for neutrophil proteinase 4. Production and
 A: Reference number: S10605; MUID:91025622
 A: Accession number: S10605
 A: Molecule type: protein
 A: Residues: 28-52 <OHL>
 R: Luedemann, J.; Utecht, B.; Gross, W.L.
 J. Exp. Med. 171, 357-362, 1990
 A: Title: Anti-neutrophil cytoplasm antibodies in Wegener's granulomatosis recognize
 A: Reference number: PL0230; MUID:90111630
 A: Accession number: PL0230
 A: Molecule type: protein
 A: Residues: 28-37, 'X', 39-40, 'I', 41-43 <LUE>
 C: Cross-references: GB:W5154; NID:9187398; PIDN:AAA59558.1; PID:9187399
 A: Note: This polymorphonuclear leukocyte serine protease from azurophilic granule
 C: Genbank: GB:W5154
 A: Cross-references: GB:W5154; NID:9187398; PIDN:AAA59558.1; PID:9187399
 A: Map position: 19p13.3-19p13.3
 A: Intons: 21/1; 76/2; 123/3; 200/3
 C: Superfamily: trypsin; trypsin homology
 C: Keyword: glycoprotein; hydrolase; polymorphonuclear leukocyte; serine proteinase
 F: 123/Domain: signal sequence status predicted <SIG>
 F: 25/Domain: propeller status predicted <PRO>
 F: 28-35/Domain: trypsin homology <TRY>
 F: 28-35/Domain: trypsin homology <TRY>
 F: 56-72, 152-209, 182-188, 199-224/Disulfide bonds: status predicted
 F: 71, 118, 203/Active site: His, Asp, Ser status predicted
 F: 129, 174/Binding site: carbohydrate (asn) (covalent) status predicted
 Query Match 67.4%; Score 93; Ds 1; Length 256;
 Best Local Similarity 64.0%; Pred. No. 1.6e-06;
 Matches 16; Conservative 2; Mismatches 7; Indels 0; Caps 0;
 Oy 1 NCGHRCGALIHPRVLTAAACLR 74
 Db 50 NCGHRCGALIHPRVLTAAACLR 74
 RESULT 4
 TRPCTR
 trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
 N: Contains: trypsinogen
 C: Species: Sus scrofa domestica (domestic pig)
 C: Date: 24-Apr-1984 (sequence revision 24-Apr-1984) text change 31-Mar-2000
 C: Author: M. A. Ballester, J. G. Nebreda, J. R. Hoidal, J. R. Gray, W. R. Gray, B. H. Hoidal, J. R.
 R: Charles, M. A. Ballester, J. G. Nebreda, J. R. Hoidal, J. R. Gray, W. R. Gray, B. H. Hoidal, J. R.
 Biochim. Biophys. Acta 69, 115-120, 1963
 A: Title: Su le trypsinogene et la trypsin de porc.
 A: Reference number: A90641
 A: Accession number: A90641
 A: Molecule type: protein
 A: Residues: 1-10 <CHA>
 R: Hemmings, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.
 Biochemistry 12, 3145-3155, 1973
 A: Title: Determination of the amino acid sequence of porcine trypsin by sequenator
 A: Reference number: A90188; MUID:7328692
 A: Accession number: A90188
 A: Molecule type: protein
 A: Residues: 9-231 <HER>
 A: Note: at position 20, Ile and Val occur alternatively
 C: Superfamily: trypsin; trypsin homology
 C: Keyword: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase;
 F: 1-231/Product: trypsinogen status experimental <ZYM>
 F: 1-231/Product: trypsinogen status experimental <ZYM>
 F: 1-231/Product: trypsinogen status experimental <ZYM>
 F: 1-231/Product: trypsinogen status experimental <ZYM>

P:7-222/Domain: trypsin homology <TRY>
 F:7-131,132-239/Product: alpha-trypsin (status experimental <MPT>
 F:6-7/Cleavage site: Lys-116 (enteropeptidase) (status experimental
 F:13-143,31-47,115-216,122-189,154-168,179-203/Disulfide bonds: (status experimental
 F:46,90,183/Active site: His, Asp, Ser (status experimental
 F:59,60,63,68/Binding site: calcium (Glu, Asn, Val, Glu) (status experimental
 F:131-132/Cleavage site: Lys-Ser (autolytic) (status experimental

Query Match 60.9% Score 84: DB 1: Length 229:
 Best Local Similarity 52.0% Pred. No. 3.2e-05:
 Matches 13: Conservative 9; Mismatches 3; Indels 0; Gaps 0:

OY 1 NOGHRFCGALIHARFVMTAASCFQ 25
 DB 25 NSGYHFCGSLINQWVVAHACY 49

RESULT 9
 trypsin (EC 3.4.21.4) II precursor - Atlantic salmon (fragment)
 C:Species: Salmo salar (Atlantic salmon)
 C:Date: 22-Nov-1993 (sequence_revision 03-Aug-1995 (text_change 22-Jun-1999
 C:Accession: S66558; S31778
 R:Mole, R.; Lorenz, J.B.; Smalleg, A.O.; Torrisen, K.R.
 R:Mole, R.; Blochem, 237, 677-685, 1995
 A:Title: Molecular cloning and characterization of anionic and cationic variants of try
 A:Reference number: S66557; M01D:96035908
 A:Accession: S66558
 A:Molecule type: mRNA
 A:Residues: 1-231 <MPT>
 A:Cross-references: EMBL:X54703; NID:964385; PIDN:CAA49676.1; PID:964386
 C:Superfamily: trypsin: trypsin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-4/Domain: signal sequence (fragment) (status predicted <SIG>
 F:5-9/Domain: activation peptide (status predicted <APT>
 F:10-231/Product: trypsin II (status predicted <MPT>
 F:10-224/Domain: trypsin homology <TRY>
 F:16-145,34-50,118-218,125-191,156-170,181-205/Disulfide bonds: (status predicted
 F:49,93,185/Active site: His, Asp, Ser (status predicted

Query Match 60.9% Score 84: DB 2: Length 231:
 Best Local Similarity 52.0% Pred. No. 3.2e-05:
 Matches 13: Conservative 7; Mismatches 5; Indels 0; Gaps 0:

OY 1 NOGHRFCGALIHARFVMTAASCFQ 25
 DB 28 NSGYHFCGSLINQWVVAHACY 52

RESULT 10
 trypsin (EC 3.4.21.4) precursor, cationic - dog

C:Species: Canis lupus familiaris (dog)
 C:Date: 30-Sep-1987 (sequence_revision 30-Sep-1987 (text_change 18-Jun-1999
 C:Accession: B26273
 R:Plinsky, S.D.; LaForge, K.S.; Scheele, G.
 M01, Cell, Biol. 5, 2669-2676, 1985
 A:Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA sequ
 A:Reference number: A26273; M01D:86284628
 A:Accession: B26273
 A:Molecule type: mRNA
 A:Residues: 1-231 <MPT>
 A:Cross-references: CB:M1590; NID:9164096; PIDN:AAA30900.1; PID:9164097
 C:Superfamily: trypsin: trypsin homology
 C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
 F:1-15/Domain: signal sequence (status predicted <SIG>
 F:16-23/Domain: activation peptide (status predicted <APT>
 F:24-246/Product: trypsin, cationic (status predicted <ENZ>
 F:24-239/Domain: trypsin homology <TRY>
 F:30-160,48-64,133-233,139-206,171-185/Disulfide bonds: (status predicted

F:63,107,200/Active site: His, Asp, Ser (status predicted
 F:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) (status predicted

Query Match 60.9% Score 84: DB 1: Length 246:
 Best Local Similarity 52.0% Pred. No. 3.4e-05:
 Matches 13: Conservative 9; Mismatches 3; Indels 0; Gaps 0:

OY 1 NOGHRFCGALIHARFVMTAASCFQ 25
 DB 42 NSGYHFCGSLINQWVVAHACY 66

RESULT 11

trypsin (EC 3.4.21.4) - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 02-Dec-1993 (sequence_revision 03-Aug-1995 (text_change 22-Jun-1999
 C:Accession: S13813; S13813
 R:Heuvelink, A.E.; Blocker, C.; Gulliksen, P.; Toullec, R.; Pulgarin, A.
 R:Heuvelink, A.E.; Blocker, C.; Gulliksen, P.; Toullec, R.; Pulgarin, A.
 A:Title: Isolation and nucleotide sequence of cDNA clone for bovine pancreatic anion
 A:Reference number: S13813; M01D:91065383
 A:Accession: S13813
 A:Molecule type: mRNA
 A:Residues: 1-247 <MPT>
 A:Cross-references: EMBL:X54703; NID:9829; PIDN:CAA38513.1; PID:9830
 C:Superfamily: trypsin: trypsin homology
 C:Keywords: hydrolase; protein digestion; serine proteinase
 F:1-15/Domain: signal sequence (status predicted <SIG>
 F:16-23/Domain: activation peptide (status predicted <APT>
 F:24-200/Product: trypsin (status predicted <ENZ>
 F:63,107,200/Active site: His, Asp, Ser (status predicted

Query Match 60.9% Score 84: DB 2: Length 247:
 Best Local Similarity 56.0% Pred. No. 3.4e-05:
 Matches 14: Conservative 7; Mismatches 4; Indels 0; Gaps 0:

OY 1 NOGHRFCGALIHARFVMTAASCFQ 25
 DB 42 NSGYHFCGSLINQWVVAHACY 66

RESULT 12

trypsin (EC 3.4.21.4) precursor, cationic - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 (sequence_revision 30-Jun-1988 (text_change 22-Jun-1999
 C:Accession: A27547
 R:Pletcher, T.S.; Albedeff, M.; Craik, C.S.; Larmann, C.
 Biochemistry 26, 3081-3086, 1987
 A:Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen.
 A:Reference number: A27547; M01D:B7271609
 A:Accession: A27547
 A:Molecule type: mRNA
 A:Residues: 1-247 <MPT>
 A:Cross-references: CB:M16524; NID:9206498; PIDN:AAA4985.1; PID:9206499
 C:Superfamily: trypsin: trypsin homology
 C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
 F:25-240/Domain: trypsin homology <TRY>
 F:31-161,49-65,133-234,140-207,172-186/Disulfide bonds: (status predicted
 F:64,108,201/Active site: His, Asp, Ser (status predicted
 F:76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) (status predicted

Query Match 60.9% Score 83: DB 2: Length 247:
 Best Local Similarity 52.0% Pred. No. 4.8e-05:
 Matches 13: Conservative 9; Mismatches 3; Indels 0; Gaps 0:

OY 1 NOGHRFCGALIHARFVMTAASCFQ 25
 DB 43 NSGYHFCGSLINQWVVAHACY 67

F:1-33/Domain: activation peptide (fragment) #status experimental <AP>
 F:34-117/118-225/226-455/Product: plasmin (fragments) #status experimental <MAT>
 F:316-114/Domain: kringle homology <KR>
 F:118-225/Product: miniplasminogen #status experimental <MIN>
 F:126-205/Domain: kringle homology <KR>
 F:226-455/Domain: plasmin chain B #status experimental <BCB>
 F:267-310/405/Active site: His, Asp, Ser #status predicted

Query Match 59.44; Score 82; DB 2; Length 455;
 Best Local Similarity 60.94; Pred. No. 0.00011;
 Matches 14; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 0Y 3 GRHFGCALIHARPPPTASCPQ 25
 DB 248 GRHFCGTLISPEWLNANLLE 270

Search completed: April 5, 2002, 15:00:25
 Job time: 159 sec

Best Local Similarity 100.0%; Pred. No. 1,3e-14;
Matches 23: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 NOGHRFCGALIHAFVPTASCFQ 25
46 NOGHRFCGALIHAFVPTASCFQ 70

RESULT 2

CAP7_PIG STANDARD: PRT: 219 AA.

AC P80015;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE AUCUCIDIN (CATIONIC ANTIMICROBIAL PROTEIN CAP37) (HEPARIN-BINDING
PROTEIN) (HBP).
OS Sus scrofa (Pig).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

RA TISSUE-Neutrophils;
RC MEDLINE-9122149; PubMed-2026172;
RA Piodgaard H., Oestergaard E., Bayne S., Svendsen A., Thomsen J.,
Engels M., Møllmer A.;
RT Covalent structure of two novel neutrophil leucocyte-derived
proteins of porcine and human origin. Neutrophilic elastase homologues
with strong homology and distinct chemotactic activities.*
RT J Biol Chem 270:5473-5477, 1995.
CC -1- FUNCTION: THIS IS A NEUTROPHIL GRANULE-DEPENDED ANTIBACTERIAL AND
MONOCYTE- AND FIBROBLAST-SPECIFIC CHEMOTACTIC GLYCOPROTEIN. BINDS
HEPARIN.

CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC PIR: S15393; TRPSIN.

DR MEROPS: S01.971; .;
DR MEROPS: P0160; 1A55.
DR INTERPRO: IPR00124; Trypsin.
DR Pfam: PF00089; Trypsin.
DR PRINTS: PR00723; CHYMOTRYPSIN.
DR SMART: SM00240; TRYP_SPE: 1.
DR PROSITE: PS00144; TRYP_SIN_DOM: 1.
DR PROSITE: PS00135; TRYP_SIN_SER: FALSE_NEG.
KM Serine protease homolog; Glycoprotein; Chemotaxis; Antibiotic;
HEPARIN BINDING;
NM CAP0015; 113 N-LINKED (GLCNAc . . .)
NM CAP0015; 144 N-LINKED (GLCNAc . . .)
FT DISULFID 126 42 BY SIMILARITY.
FT DISULFID 152 158 BY SIMILARITY.
SO SEQUENCE 219 AA; 24301 MW; 99129CAB8B0749D CRC64;

Query Match 74.6%; Score 103; DB 1; Length 219;

Best Local Similarity 75.0%; Pred. No. 3,6e-09;
Matches 18: Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 2 OCHRGCGALIHAFVPTASCFQ 25
21 OCHRGCGALIHAFVPTASCFQ 44

RESULT 3

PRN3_HUMAN STANDARD: PRT: 256 AA.

AC P24158; P15637;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1996 (Rel. 37, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MYELOBLASTIN PRECURSOR (PC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3)
DE (PRN3) (AGP7) (WEGENER'S AUTOANTIGEN) (P25) (C-ANCA ANTIGEN).
OS PRN3 OR MBN.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-9203028; PubMed-1681549;
RA Labbaye C, Musclet P, Cayre Y E;
RT "Wegener autoantigen and myeloblastin are encoded by a single mRNA.*"
RL Proc. Natl. Acad. Sci. U.S.A. 88:9253-9256(1991).

RA SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skovronski E., Adamson A.W.,
Burkhardt-Schultz K.J., Gordon L., Kyle A., Ramirez M., Stillwagen S.,
Phan H., Velasco N., De L., Regula W., Terry A., Barnes J.,
Bengham L., Poundstone P., Christensen M., Georgescu A., Avila J.,
Cie S., Atlix C., Andraese F., Frankheim M., Amico Keller G.,
Cie S., Duffell J., Luckeney R., Bruce R., Thomas P., Quan G.,
Kronmiller B., Mellano A., Williams M., On D., Nolan M., Strong S.,
Kobayashi A., Olsen A.S., Carrano A.V., On D., Nolan M., Strong S.,
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE OF 2-256 FROM N.A.; AND SEQUENCE OF 48-71 AND 156-181.
RA MEDLINE-9107974; PubMed-2258701;
RA Campanelli D., Melchior M., Fu Y., Nakata M., Shuman H., Nathan C.,
Gabay J.E.;
RT Cloning of cDNA for proteinase 3: a serine protease, antibiotic, and
autolysin from human neutrophils.*
RT J Exp. Med. 172:1709-1715(1990).

RA SEQUENCE OF 1-20 AND 22-256 FROM N.A.
RA MEDLINE-92390417; PubMed-1518649;
RA Zimmer M., Medcalf R.L., Fink T.M., Matmann C., Lichter P.,
Jeune D.E.;
RT "Three human elastase-like genes coordinately expressed in the
myelomonocyte lineage are organized as a single genetic locus on
19pter.*"
RT Proc. Natl. Acad. Sci. U.S.A. 89:8215-8219(1992).

RA SEQUENCE OF 43-256 FROM N.A.
RA MEDLINE-9090623; PubMed-1592637;
RA Bories D, Raynal M-C, Solomon D.H., Derjanykiewicz Z., Cayre Y E;
RT "Down-regulation of a serine protease, myeloblastin, causes growth
arrest and differentiation of promyelocytic leukemia cells.*"
RL Cell 59:959-968(1989).

RA SEQUENCE OF 28-67 AND 228-244.
RA MEDLINE-91236723; PubMed-203050;
RA Rao N.V., Wehner N.G., Marshall B.C., Gray M.R., Gray B.H.,
Fidel M.;
RT "Cloning and characterization of proteinase-3 (PR-3), a neutrophil serine
protease. Structural and functional properties.*"
RL J. Biol. Chem. 266:9540-9548(1991).

RA SEQUENCE OF 28-47.
RA MEDLINE-89315847; PubMed-2501794;
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
Marrs M.N., Seeger M., Nathan C.F.;
RT "Antibiotic proteins of human polymorphonuclear leukocytes.*"
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).

RA SEQUENCE OF 28-47 AND 196-219.
RA MEDLINE-90130450; PubMed-2444977;
RA Wilde C.G., Snoble J., Griffith J.E., Scott R.W.;
RT "Characterization of two azurophilic granule proteinases with active site
homology to neutrophil elastase.*"
RL J. Biol. Chem. 265:2038-2041(1990).

[9]
SEQUENCE OF 28-48, AND IDENTITY OF WEGENER'S AUTOANTIGEN WITH PR-3.

Db 43 NAGYHFCGCSLINSOWWVSAHICXK 67

RESULT 14

TR12_CHICK

AC 090627

DT 01-NOV-1997 (Rel. 35, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE TRYPsin I-P1 PRECURSOR (EC 3.4.21.4).

OS Gallus gallus (Chicken).

OC Euteleostomi: Metazoa: Chordata: Vertebrata: Euteleostomi: Archosauria: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae: Gallus.

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

Db 44 NSGYHFCGCSLINSOWVISAHICXK 68

RESULT 15

TR12_CHICK

AC 090627

DT 01-NOV-1997 (Rel. 35, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE TRYPsin I-P1 PRECURSOR (EC 3.4.21.4).

OS Gallus gallus (Chicken).

OC Euteleostomi: Metazoa: Chordata: Vertebrata: Euteleostomi: Archosauria: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae: Gallus.

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

NCB1_TaxID=9031

Query Match 60.1% Score 83: DB 1: Length 248:
Best Local Similarity 52.0% Pred. No. 5.7e-06:
Matches 13: Conservative 8: Mismatches 4: Indels 0: Gaps 0:

CC This SNIS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL: U5155; M479912.1;
CC HSP: P00763; IDPO.
CC MEROPS: S01.151;
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR001254; Trypsin.
CC Pfam: PF00089; Trypsin.1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC SMART: SM00020; TRYP-SPEC.1.
CC PROSITE: PS00144; TRYPsin_DOM.1.
CC PROSITE: PS00135; TRYPsin_HIS.1.
CC PROSITE: PS00135; TRYPsin_SER.1.
CC Hydrolase: Serine protease; Digestion; Pancreas; Zymogen; Signal;
CC Multigene family.
CC SIGNAL 1 15
CC PROPEP 16 25
CC ACT_SITE 26 248
CC ACT_SITE 65 65
CC ACT_SITE 109 109
CC ACT_SITE 202 202
CC DISULFID 32 162
CC DISULFID 50 66
CC DISULFID 134 235
CC DISULFID 141 235
CC DISULFID 171 235
CC DISULFID 198 235
CC DISULFID 222 235
CC SITE 196 196
CC SITE 248 AA: 26069 MW: C4CF589912B3D98 CRC64:
CC REQUIRED FOR SPECIFICITY (BY SIMILARITY).

CC This SNIS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL: U5155; M479912.1;
CC HSP: P00763; IDPO.
CC MEROPS: S01.151;
CC InterPro: IPR001314; Chymotrypsin.
CC InterPro: IPR001254; Trypsin.
CC Pfam: PF00089; Trypsin.1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC SMART: SM00020; TRYP-SPEC.1.
CC PROSITE: PS00144; TRYPsin_DOM.1.
CC PROSITE: PS00135; TRYPsin_HIS.1.
CC PROSITE: PS00135; TRYPsin_SER.1.
CC Hydrolase: Serine protease; Digestion; Pancreas; Zymogen; Signal;
CC Multigene family.
CC SIGNAL 1 15
CC PROPEP 16 25
CC ACT_SITE 26 248
CC ACT_SITE 65 65
CC ACT_SITE 109 109
CC ACT_SITE 202 202
CC DISULFID 32 162
CC DISULFID 50 66
CC DISULFID 134 235
CC DISULFID 141 235
CC DISULFID 171 235
CC DISULFID 198 235
CC DISULFID 222 235
CC SITE 196 196
CC SITE 248 AA: 26069 MW: 78B79D56F515P0C CRC64:
CC REQUIRED FOR SPECIFICITY (BY SIMILARITY).

Query Match 60.1% Score 83: DB 1: Length 248:
Best Local Similarity 52.0% Pred. No. 5.7e-06:
Matches 13: Conservative 8: Mismatches 4: Indels 0: Gaps 0:

[illegible][illegible]

DR InterPro: IPR001314: Chymotrypsin.
 DR InterPro: IPR000001: Kringle.
 DR InterPro: IPR003014: PAN.
 DR InterPro: IPR003609: Pen_app.
 DR InterPro: IPR001254: Trypsin.
 DR Pfam: PF00051: Kringle_4.
 DR Pfam: PF00024: PAN_1.
 DR Pfam: PF00054: Trypsin_1.
 DR PRINTS: PR00722: CHYMOTRYPSIN.
 DR PRINTS: PR00016: KRINGLE.
 DR SMART: SM00130: KR_4.
 DR SMART: SM00473: PAN_AP_1.
 DR SMART: SM00020: TRYSPC_1.
 DR PROSITE: PS00021: KRINGLE_1_4.
 DR PROSITE: PS00070: KRINGLE_2_4.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 483 POTENTIAL.
 FT CDS 19 483 MACROPHAGE-STIMULATING PROTEIN.
 FT CDS 484 711 MACROPHAGE-STIMULATING PROTEIN.
 SO SEQUENCE 711 AA: 60353 MW: 2481500DaOJ1f06 CRC64;

Query Match 60.1% Score 83; DB 4; Length 711;
 Best Local Similarity 52.2%; Pred. No. 3.4e-05;
 Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
 QY 2 QGNRCGGALHARFVTATASCP 24
 DB 502 QGNRCGGSLAKEDWILTAACP 524

Search completed: April 5, 2002, 15:00:56
 Job time: 160 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OH protein - protein search, using SW model

Run on: April 5, 2002, 14:56:16 : Search time 12.45 Seconds

(without alignments)
45.187 Million cell updates/sec

Title: US-09-657-276-1032

Perfect score: 138RPFCCGMLHARVMTASCFQ 25

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 01

Maximum Match 1000

Listing first 45 summaries

Database:

Issued: Patents, AA.*

1: /cgn2.6/pdata/2/1aa/5A_COMB.pep.*

2: /cgn2.6/pdata/2/1aa/5B_COMB.pep.*

3: /cgn2.6/pdata/2/1aa/5A_COMB.pep.*

4: /cgn2.6/pdata/2/1aa/5B_COMB.pep.*

5: /cgn2.6/pdata/2/1aa/PCRU5_COMB.pep.*

6: /cgn2.6/pdata/2/1aa/heckfile1.pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the hit being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	25	1	US-07-969-931-8
2	138	100.0	25	1	US-08-931-158-1
3	138	100.0	25	1	US-08-931-158-1
4	138	100.0	25	1	US-08-931-158-1
5	138	100.0	25	2	US-08-931-158-1
6	138	100.0	25	2	US-08-931-158-1
7	138	100.0	25	2	US-08-931-158-1
8	138	100.0	25	2	US-08-931-158-1
9	138	100.0	25	2	US-08-931-158-1
10	138	100.0	25	2	US-08-931-158-1
11	138	100.0	25	2	US-08-931-158-1
12	138	100.0	25	2	US-08-931-158-1
13	138	100.0	25	2	US-08-931-158-1
14	138	100.0	25	2	US-08-931-158-1
15	138	100.0	25	2	US-08-931-158-1
16	138	100.0	25	2	US-08-931-158-1
17	138	100.0	25	2	US-08-931-158-1
18	138	100.0	25	2	US-08-931-158-1
19	138	100.0	25	2	US-08-931-158-1
20	138	100.0	25	2	US-08-931-158-1
21	138	100.0	25	2	US-08-931-158-1
22	138	100.0	25	2	US-08-931-158-1
23	138	100.0	25	2	US-08-931-158-1
24	138	100.0	25	2	US-08-931-158-1
25	138	100.0	25	2	US-08-931-158-1
26	138	100.0	25	2	US-08-931-158-1
27	138	100.0	25	2	US-08-931-158-1

28	124	88.9	25	3	US-09-258-934-17	Sequence 17, App1
29	124	88.9	25	3	US-09-258-934-17	Sequence 20, App1
30	124	88.9	25	3	US-09-258-934-17	Sequence 15, App1
31	124	88.9	25	3	US-09-258-934-17	Sequence 16, App1
32	123	88.1	25	3	US-09-258-934-17	Sequence 19, App1
33	123	88.1	25	3	US-09-258-934-17	Sequence 30, App1
34	122	88.4	25	3	US-09-258-934-17	Sequence 31, App1
35	122	88.4	25	3	US-09-258-934-17	Sequence 33, App1
36	122	88.4	25	3	US-09-258-934-17	Sequence 34, App1
37	122	88.4	25	3	US-09-258-934-17	Sequence 35, App1
38	118	85.5	25	3	US-09-258-934-17	Sequence 7, App1
39	116	84.1	25	3	US-09-258-934-17	Sequence 32, App1
40	116	84.1	25	3	US-09-258-934-17	Sequence 35, App1
41	116	84.1	25	3	US-09-258-934-17	Sequence 7, App1
42	116	84.1	25	3	US-09-258-934-17	Sequence 7, App1
43	116	84.1	25	3	US-09-258-934-17	Sequence 7, App1
44	116	84.1	25	3	US-09-258-934-17	Sequence 7, App1
45	110	79.7	20	2	US-08-931-158-1	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-07-969-931-8
Sequence 8, Application US-07969931
Patent No. 5458874
GENERAL INFORMATION:
APPLICANT: Seltmann, Helmut
TITLE OF INVENTION: Chemotactic Antibiotic and
TITLE OF INVENTION: Lipopolysaccharide-Binding Peptide Fragments of CAP37
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Needle & Rosenberg, P.C.
STREET: 133 Carnegie Way N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-07/969,931
FILING DATE: 19921030
PRIORITY APPLICATION DATA: US 07/543,151
PRIORITY APPLICATION NUMBER: 07/543,151
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/375,739
FILING DATE: 05-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Severson, Mary L.
REGISTRATION NUMBER: 34,927
REFERENCE/DOCKET NUMBER: 0510.024
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-0770
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal
ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
US-07-969-931-8

```

: STREET: 9400 No. 5627262th Broadway, Suite 420
: CITY: Oklahoma City
: STATE: Oklahoma
: COUNTRY: United States of America
: ZIP: 73114
: COMPUTER READABLE FORM:
: 3.5, 1.44 Mb High Density Diskette
: OPERATING SYSTEM: MS-DOS 5.00
: SOFTWARE: WordPerfect 5.1 (saved in ASCII format)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,328
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/235,399
: FILING DATE: April 29, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,931
: FILING DATE: October 30, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/855,417
: FILING DATE: March 18, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/543,151
: FILING DATE: June 25, 1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/375,739
: FILING DATE: July 5, 1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Corbett, Christopher W., Ph.D.
: REGISTRATION NUMBER: 36,109
: REFERENCE/DOCKET NUMBER: 5820,360
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 405-478-5344
: TELEFAX: 405-478-5349
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
: US-08-482,328-1

Query Match 100.0%; Score 138; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 8,3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NCGRRFCGALIHARVMTASCFO 25
DB 1 NCGRRFCGALIHARVMTASCFO 25

RESULT 5
US-08-840-519-1
: Sequence 1, Application US/08840519
: Patent No. 5877151
: GENERAL INFORMATION:
: APPLICANT: Pereira, Heloise Anne
: TITLE OF INVENTION: Method and Composition for The Treatment
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Christopher W. Corbett, Ph.D.
: ADDRESS: Dunlap & Coddling, P.C.
: STREET: 9400 No. 5877151th Broadway, Suite 420
: CITY: Oklahoma City
: STATE: Oklahoma
: COUNTRY: United States of America
: ZIP: 73114
: COMPUTER READABLE FORM:
: 3.5, 1.44 Mb High Density Diskette
: OPERATING SYSTEM: MS-DOS 5.00
: SOFTWARE: WordPerfect 5.1 (saved in ASCII format)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/840,519
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/482,328
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: 08/235,399
: FILING DATE: April 29, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,931
: FILING DATE: October 30, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/855,417
: FILING DATE: March 18, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/543,151
: FILING DATE: June 25, 1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/375,739
: FILING DATE: July 5, 1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Corbett, Christopher W., Ph.D.
: REGISTRATION NUMBER: 36,109
: REFERENCE/DOCKET NUMBER: 5820,360
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 405-478-5344
: TELEFAX: 405-478-5349
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
: US-08-840-519-1

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5, 1.44 Mb High Density Diskette
: COMPUTER: IBM AT Compatible
: OPERATING SYSTEM: MS-DOS 5.00
: SOFTWARE: WordPerfect 5.1 (saved in ASCII format)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/657,276
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/482,328
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: 08/235,399
: FILING DATE: April 29, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,931
: FILING DATE: October 30, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/855,417
: FILING DATE: March 18, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/543,151
: FILING DATE: June 25, 1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/375,739
: FILING DATE: July 5, 1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Corbett, Christopher W., Ph.D.
: REGISTRATION NUMBER: 36,109
: REFERENCE/DOCKET NUMBER: 5820,360
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 405-478-5344
: TELEFAX: 405-478-5349
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
: US-08-840-519-1

Query Match 100.0%; Score 138; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 8,3e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NCGRRFCGALIHARVMTASCFO 25
DB 1 NCGRRFCGALIHARVMTASCFO 25

RESULT 6
US-09-260-373-1
: Sequence 1, Application US/09260373
: Patent No. 6071879
: GENERAL INFORMATION:
: APPLICANT: Pereira, Heloise Anne
: TITLE OF INVENTION: Method and Composition for The Treatment
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Christopher W. Corbett, Ph.D.
: ADDRESS: Dunlap & Coddling, P.C.
: STREET: 9400 No. 6071879th Broadway, Suite 420
: CITY: Oklahoma City
: STATE: Oklahoma
: COUNTRY: United States of America
: ZIP: 73114
: COMPUTER READABLE FORM:
: 3.5, 1.44 Mb High Density Diskette
: OPERATING SYSTEM: MS-DOS 5.00
: SOFTWARE: WordPerfect 5.1 (saved in ASCII format)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/260,373
: FILING DATE: Filed Herewith
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/482,328
: FILING DATE: 07-JUN-1995
: APPLICATION NUMBER: 08/235,399
: FILING DATE: April 29, 1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/969,931
: FILING DATE: October 30, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/855,417
: FILING DATE: March 18, 1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/543,151
: FILING DATE: June 25, 1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/375,739
: FILING DATE: July 5, 1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Corbett, Christopher W., Ph.D.
: REGISTRATION NUMBER: 36,109
: REFERENCE/DOCKET NUMBER: 5820,360
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 405-478-5344
: TELEFAX: 405-478-5349
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 25 amino acids
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: ORIGINAL SOURCE: 20-44aa of mature CAP37 protein
: US-08-840-519-1

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Spitznagel, John K.
FILING DATE: 19921030
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/543,151
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/375,739
FILING DATE: 05-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Severson, Mary L.
REFERENCE/DOCKET NUMBER: 0510.024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-07-855-417A-9

Query Match 100.0%; Score 138; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 6, 9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRRFCGALIHARFVMTASCFQ 25
DB 20 NOGRRFCGALIHARFVMTASCFQ 44

RESULT 10
US-07-855-417A-9
Sequence 9, Application US/07855417A
Patent No. 5484885
GENERAL INFORMATION:
APPLICANT: Pereira, Heloise Anne
TITLE OF INVENTION: Chemotactic, Antidiabetic and
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Lawrence E. Rosenberg, P.C.
STREET: 113 Carnegie Way N.W., Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/855,417A
FILING DATE: 18-MAR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/543,151
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/375,739
FILING DATE: 05-JUL-1989

ATTORNEY/AGENT INFORMATION:
NAME: Severson, Mary L.
REGISTRATION NUMBER: 34,927
REFERENCE/DOCKET NUMBER: 0510.024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-07-855-417A-9

Query Match 100.0%; Score 138; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 6, 9e-13;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NOGRRFCGALIHARFVMTASCFQ 25
DB 20 NOGRRFCGALIHARFVMTASCFQ 44

RESULT 11
US-08-491-204A-18
Sequence 18, Application US/08491204A
Patent No. 5897247
GENERAL INFORMATION:
APPLICANT: Josephson, Joost B.
APPLICANT: Chertov, Oleg
APPLICANT: Michel, Dennis F.
APPLICANT: Xu, Luoling
APPLICANT: Wang, Ji Ming
APPLICANT: Murphy, William J.
APPLICANT: Longo, Dan L.
TITLE OF INVENTION: CHEMOTACTIC AGENTS FOR T-CELLS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 77 Cambridge Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08491,204A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15260
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-491-204A-18

US-09-258-934-37

Query Match 97.8%; Score 135; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 2, 2e-13;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOGHRFCGALIHARFVTMA SCFQ 25
|||||
DB 1 NOGHRFCGALIHARFVTMA SCFQ 25

Search completed: April 5, 2002, 15:00:06
Job time: 230 sec